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SEQUENCE LISTING

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<140> 09/626,813  
<141> 2000-07-27  
<150> 60/146,580  
<151> 1999-07-30  
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Xaa  
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<210> 24  
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Asp Thr Ala Ser Lys Leu Xaa Asp Glu Ala Ala Phe Lys Val Thr Glu  
20 25 30

Asp Gly Met Arg  
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gaaaatgaat ttataatgaa ggcagaggga gaaACCCAGG aagttgagat aaagctaact 540  
cttgaagatg agggattatt ggacatcgag gttcaagagg agacaaagag cgcatatgga 600  
gtcagctatc tctccgacat ggttaaaggc cttggaaagg ccgatgaagt tacaataaag 660  
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20 25 30

Glu Asp Gly Ile Ser Met Arg Ala Met Asp Pro Ser Arg Val Val Leu  
35 40 45

Ile Asp Leu Asn Leu Pro Ser Ser Ile Phe Ser Lys Tyr Glu Val Val  
50 55 60

Glu Pro Glu Thr Ile Gly Val Asn Met Asp His Leu Lys Lys Ile Leu  
65 70 75 80

Lys Arg Gly Lys Ala Lys Asp Thr Leu Ile Leu Lys Lys Gly Glu Glu  
85 90 95

Asn Phe Leu Glu Ile Thr Ile Gln Gly Thr Ala Thr Arg Thr Phe Arg  
100 105 110

Val Pro Leu Ile Asp Val Glu Glu Met Glu Val Asp Leu Pro Glu Leu  
115 120 125

Pro Phe Thr Ala Lys Val Val Leu Gly Glu Val Leu Lys Asp Ala  
130 135 140

Val Lys Asp Ala Ser Leu Val Ser Asp Ser Ile Lys Phe Ile Ala Arg  
145 150 155 160

Glu Asn Glu Phe Ile Met Lys Ala Glu Gly Glu Thr Gln Glu Val Glu  
165 170 175

Ile Lys Leu Thr Leu Glu Asp Glu Gly Leu Leu Asp Ile Glu Val Gln  
180 185 190

Glu Glu Thr Lys Ser Ala Tyr Gly Val Ser Tyr Leu Ser Asp Met Val  
195 200 205  
Lys Gly Leu Gly Lys Ala Asp Glu Val Thr Ile Lys Phe Gly Asn Glu  
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225 230 235 240  
Phe Leu Leu Ala Pro Arg Val Glu Glu  
245

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tttctctgt tcagttatng ccttagataa gcttaataat actttgatac ctttcttagt 180  
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sequence of the genomic RFC clone

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<223> Xaa is any amino acid

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Asp Leu Xaa Phe Phe Leu Leu Phe Phe Cys Ser Val Xaa Ala Asp Lys  
35 40 45

Leu Asn Asn Thr Leu Ile Pro Phe Leu Val Val Cys Glu Ser Met Ser  
50 55 60

Glu Glu Ile Arg Glu Val Lys Val Leu Glu Lys Pro Trp Val Glu Lys  
65 70 75 80

Tyr Arg Pro Gln Arg Leu Asp Asp Ile Val Gly Gln Glu His Ile Val  
85 90 95

Lys Arg Leu Lys His Tyr Val Lys Thr Gly Ser Met Pro His Leu Leu  
100 105 110

Phe Ala Gly Pro Pro Gly Val Gly Lys Cys Leu Thr Gly Asp Thr Lys  
115 120 125

Val Ile Ala Asn Gly Gln Leu Phe Glu Leu Gly Glu Leu Val Glu Lys  
130 135 140

Leu Ser Gly Gly Arg Phe Gly Pro Thr Pro Val Lys Gly Leu Lys Val  
145 150 155 160

Leu Gly Ile Asp Glu Asp Gly Lys Leu Arg Glu Phe Glu Val Gln Tyr  
165 170 175

Val Tyr Lys Asp Arg Thr Asp Arg Leu Ile Lys Ile Lys Thr Gln Leu  
180 185 190

Gly Arg Glu Leu Lys Val Thr Pro Tyr His Pro Leu Leu Val Ile Gly  
195 200 205

Glu Asn Gly Glu Leu Lys Trp Ile Lys Ala Glu Glu Leu Lys Leu Gly  
210 215 220

Asp Lys Leu Ala Ile Pro Ser Phe Leu Pro Leu Ile Thr Gly Glu Asn  
225 230 235 240

Pro Leu Ala Glu Trp Leu Gly Tyr Phe Met Gly Ser Gly Tyr Ala Tyr  
245 250 255

Pro Lys Asn Ser Val Ile Thr Phe Thr Asn Glu Asp Pro Leu Ile Arg

260

265

270

Gln Arg Phe Met Glu Leu Thr Glu Lys Leu Phe Pro Asp Ala Lys Ile  
 275 280 285

Arg Glu Arg Ile His Ala Asp Gly Thr Pro Glu Val Tyr Val Val Ser  
 290 295 300

Arg Lys Ala Trp Ser Leu Val Asn Ser Ile Ser Leu Thr Leu Ile Pro  
 305 310 315 320

Arg Glu Gly Trp Lys Gly Ile Arg Ser Phe Leu Arg Ala Tyr Ser Asp  
 325 330 335

Cys Asn Gly Arg Ile Glu Ser Asp Ala Ile Val Leu Ser Thr Asp Asn  
 340 345 350

Asn Asp Met Ala Gln Gln Ile Ala Tyr Ala Leu Ala Ser Phe Gly Ile  
 355 360 365

Ile Ala Lys Met Asp Gly Glu Asp Val Ile Ile Ser Gly Ser Asp Asn  
 370 375 380

Ile Glu Arg Phe Leu Asn Glu Ile Gly Phe Ser Thr Gln Ser Lys Leu  
 385 390 395 400

Lys Glu Ala Gln Lys Leu Ile Arg Lys Thr Asn Val Arg Ser Asp Gly  
 405 410 415

Leu Lys Ile Asn Tyr Glu Leu Ile Ser Tyr Val Lys Asp Arg Leu Arg  
 420 425 430

Leu Asn Val Asn Asp Lys Arg Asn Leu Ser Tyr Arg Asn Ala Lys Glu  
 435 440 445

Leu Ser Trp Glu Leu Met Lys Glu Ile Tyr Tyr Arg Leu Glu Glu Leu  
 450 455 460

Glu Arg Leu Lys Lys Val Leu Ser Glu Pro Ile Leu Ile Asp Trp Asn  
 465 470 475 480

Glu Val Ala Lys Lys Ser Asp Glu Val Ile Glu Lys Ala Lys Ile Arg  
 485 490 495

Ala Glu Lys Leu Leu Glu Tyr Ile Lys Gly Glu Arg Lys Pro Ser Phe  
 500 505 510

Lys Glu Tyr Ile Glu Ile Ala Lys Val Leu Gly Ile Asn Val Glu Arg  
 515 520 525

Thr Ile Glu Ala Met Lys Ile Phe Ala Lys Arg Tyr Ser Ser Tyr Ala  
 530 535 540

Glu Ile Gly Arg Lys Leu Gly Thr Trp Asn Phe Asn Val Lys Thr Ile  
 545 550 555 560

Leu Glu Ser Asp Thr Val Asp Asn Val Glu Ile Leu Glu Lys Ile Arg  
 565 570 575

Lys Ile Glu Leu Glu Leu Ile Glu Glu Ile Leu Ser Asp Gly Lys Leu  
 580 585 590

Lys Glu Gly Ile Ala Tyr Leu Ile Phe Leu Phe Gln Asn Glu Leu Tyr  
595 600 605

Trp Asp Glu Ile Thr Glu Val Lys Glu Leu Arg Gly Asp Phe Ile Ile  
610 615 620

Tyr Asp Leu His Val Pro Gly Tyr His Asn Phe Ile Ala Gly Asn Met  
625 630 635 640

Pro Thr Val Val His Asn Thr Thr Ala Ala Leu Ala Leu Ala Arg Glu  
645 650 655

Leu Phe Gly Glu Asn Trp Arg His Asn Phe Leu Glu Leu Asn Ala Ser  
660 665 670

Asp Glu Arg Gly Ile Asn Val Ile Arg Glu Lys Val Lys Glu Phe Ala  
675 680 685

Arg Thr Lys Pro Ile Gly Gly Ala Ser Phe Lys Ile Ile Phe Leu Asp  
690 695 700

Glu Ala Asp Ala Leu Thr Gln Asp Ala Gln Gln Ala Leu Arg Arg Thr  
705 710 715 720

Met Glu Met Phe Ser Ser Asn Val Arg Phe Ile Leu Ser Cys Asn Tyr  
725 730 735

Ser Ser Lys Ile Ile Glu Pro Ile Gln Ser Arg Cys Ala Ile Phe Arg  
740 745 750

Phe Arg Pro Leu Arg Asp Glu Asp Ile Ala Lys Arg Leu Arg Tyr Ile  
755 760 765

Ala Glu Asn Glu Gly Leu Glu Leu Thr Glu Glu Gly Leu Gln Ala Ile  
770 775 780

Leu Tyr Ile Ala Glu Gly Asp Met Arg Arg Ala Ile Asn Ile Leu Gln  
785 790 795 800

Ala Ala Ala Ala Leu Asp Lys Lys Ile Thr Asp Glu Asn Val Phe Met  
805 810 815

Val Ala Ser Arg Ala Arg Pro Glu Asp Ile Arg Glu Met Met Leu Leu  
820 825 830

Ala Leu Lys Gly Asn Phe Leu Lys Ala Arg Glu Lys Leu Arg Glu Ile  
835 840 845

Leu Leu Lys Gln Gly Leu Ser Gly Glu Asp Val Leu Val Gln Met His  
850 855 860

Lys Glu Val Phe Asn Leu Pro Ile Glu Glu Pro Lys Lys Val Leu Leu  
865 870 875 880

Ala Asp Lys Ile Gly Glu Tyr Asn Phe Arg Leu Val Glu Gly Ala Asn  
885 890 895

Glu Ile Ile Gln Leu Glu Ala Leu Leu Ala Gln Phe Thr Leu Ile Gly  
900 905 910

Lys Lys Ser Met Pro Glu Leu Pro Trp Val Glu Lys Tyr Arg Pro Lys  
915 920 925

Lys Leu Ser Glu Ile Val Asn Gln Glu Glu Ala Ile Glu Lys Val Arg  
930 935 940

Ala Trp Ile Glu Ser Trp Leu His Gly His Pro Pro Lys Lys Ala  
945 950 955 960

Leu Leu Leu Ala Gly Pro Pro Gly Ser Gly Lys Thr Thr Thr Val Tyr  
965 970 975

Ala Leu Ala Asn Glu Tyr Asn Phe Glu Val Ile Glu Leu Asn Ala Ser  
980 985 990

Asp Glu Arg Thr Tyr Glu Lys Ile Ser Arg Tyr Val Gln Ala Ala Tyr  
995 1000 1005

Thr Met Asp Ile Leu Gly Lys Arg Arg Lys Ile Ile Phe Leu Asp Glu  
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Ala Asp Asn Ile Glu Pro Ser Gly Ala Lys Glu Ile Ala Lys Leu Ile  
1025 1030 1035 1040

Asp Lys Ala Lys Asn Pro Ile Ile Met Ala Ala Asn Lys Tyr Trp Glu  
1045 1050 1055

Val Pro Lys Glu Ile Arg Glu Lys Ala Glu Leu Val Glu Tyr Lys Arg  
1060 1065 1070

Leu Thr Gln Arg Asp Val Met Asn Ala Leu Ile Arg Ile Leu Lys Arg  
1075 1080 1085

Glu Gly Ile Thr Val Pro Lys Glu Ile Leu Leu Glu Ile Ala Lys Arg  
1090 1095 1100

Ser Ser Gly Asp Leu Arg Ala Ala Ile Asn Asp Leu Gln Thr Val Val  
1105 1110 1115 1120

Val Gly Gly Tyr Glu Asp Ala Thr Gln Val Leu Ala Tyr Arg Asp Val  
1125 1130 1135

Glu Lys Thr Val Phe Gln Ala Leu Gly Leu Val Phe Gly Ser Asp Asn  
1140 1145 1150

Ala Lys Arg Ala Lys Met Ala Met Trp Asn Leu Asp Met Ser Pro Asp  
1155 1160 1165

Glu Phe Leu Leu Trp Val Asp Glu Asn Ile Pro His Leu Tyr Leu Asn  
1170 1175 1180

Pro Glu Glu Ile Ala Gln Ala Tyr Asp Ala Ile Ser Arg Ala Asp Ile  
1185 1190 1195 1200

Tyr Leu Gly Arg Ala Ala Arg Thr Gly Asn Tyr Ser Leu Trp Lys Tyr  
1205 1210 1215

Ala Ile Asp Met Met Thr Ala Gly Val Ala Val Ala Gly Arg Lys Arg  
1220 1225 1230

Arg Gly Phe Val Lys Phe Tyr Pro Pro Asn Thr Leu Lys Ile Leu Ala

1235

1240

1245

Glu Ser Lys Glu Glu Arg Glu Ile Arg Glu Ser Ile Ile Lys Lys Ile  
1250 1255 1260

Ile Arg Glu Met Xaa Met Ser Arg Leu Gln Ala Ile Glu Thr Met Lys  
1265 1270 1275 1280

Ile Ile Arg Glu Ile Phe Glu Asn Asn Leu Asp Leu Ala Ala His Phe  
1285 1290 1295

Thr Val Phe Leu Gly Leu Ser Glu Lys Glu Val Glu Phe Leu Ala Gly  
1300 1305 1310

Lys Glu Lys Ala Gly Thr Ile Trp Gly Lys Ala Leu Ala Leu Arg Arg  
1315 1320 1325

Lys Leu Lys Glu Leu Gly Ile Arg Glu Glu Glu Lys Pro Lys Val Glu  
1330 1335 1340

Ile Glu Glu Glu Glu Glu Glu Lys Thr Glu Glu Glu Lys Glu  
1345 1350 1355 1360

Glu Ile Glu Glu Lys Pro Glu Glu Lys Glu Glu Glu Lys Lys Glu  
1365 1370 1375

Lys Glu Lys Pro Lys Lys Gly Lys Gln Ala Thr Leu Phe Asp Phe Leu  
1380 1385 1390

Lys Lys Leu Pro Phe Phe Tyr Ser Ser Glu Ser Trp Pro Ser Asn  
1395 1400 1405

Phe Phe Tyr Cys Leu Leu His Ile Asn Leu Tyr Glu Leu Glu Phe Leu  
1410 1415 1420

Gln Pro Gly Gly Ser Thr Ser Ser Arg Ala Ala Ala Thr Ala Val Glu  
1425 1430 1435 1440

Leu Gln Leu Leu Phe Pro Leu Val Arg Val Asn Phe Glu Leu Gly Val  
1445 1450 1455

Ile Met Val Ile Ala Val Ser Cys Val Lys Leu Leu Ser Ala His Asn  
1460 1465 1470

Ser Thr Gln His Thr Asn Pro Glu Ala Ile Val Asn Pro Gly Val Pro  
1475 1480 1485

Asn Xaa Xaa Asn Ser His Leu Xaa Cys Ala His Cys Pro Leu Ser Xaa  
1490 1495 1500

Arg Glu Thr Cys Arg Ala Ser Cys Ile Asn Glu Ser Ala Asn Xaa Arg  
1505 1510 1515 1520

Gly Xaa Ala Val Ala Tyr Trp Ala Leu Phe Arg Phe Leu Ala His Asp  
1525 1530 1535

Ser Leu Arg Ser Val Xaa Gly Cys Gly Glu Arg Tyr Gln Leu Ile Lys  
1540 1545 1550

Gly Gly Asn Thr Val Ile Xaa Lys Ser Gly Asp Asn Ala Gly Lys Asn  
1555 1560 1565

Phe Xaa Gln Lys Ala Xaa Lys Gly Gly Asn Lys Ala Xaa Ser Gly Phe  
1570 1575 1580

Phe Xaa Gly Pro Pro Arg Xaa Leu Xaa Lys Ser Thr His Ser Ser Gly  
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Lys Pro Lys

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<211> 479

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Recombinant  
P55 clone

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<223> Xaa is any amino acid

<400> 63

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20 25 30

Glu Ser Trp Leu His Gly His Pro Pro Lys Lys Lys Ala Leu Leu Leu  
35 40 45

Ala Gly Pro Pro Gly Ser Gly Lys Thr Thr Thr Val Tyr Ala Leu Ala  
50 55 60

Asn Glu Tyr Asn Phe Glu Val Ile Glu Leu Asn Ala Ser Asp Glu Arg  
65 70 75 80

Thr Tyr Glu Lys Ile Ser Arg Tyr Val Gln Ala Ala Tyr Thr Met Asp  
85 90 95

Ile Leu Gly Lys Arg Arg Lys Ile Ile Phe Leu Asp Glu Ala Asp Asn  
100 105 110

Ile Glu Pro Ser Gly Ala Lys Glu Ile Ala Lys Leu Ile Asp Lys Ala  
115 120 125

Lys Asn Pro Ile Ile Met Ala Ala Asn Lys Tyr Trp Glu Val Pro Lys  
130 135 140

Glu Ile Arg Glu Lys Ala Glu Leu Val Glu Tyr Lys Arg Leu Thr Gln  
145 150 155 160

Arg Asp Val Met Asn Ala Leu Ile Arg Ile Leu Lys Arg Glu Gly Ile  
165 170 175

Thr Val Pro Lys Glu Ile Leu Leu Glu Ile Ala Lys Arg Ser Ser Gly  
180 185 190

Asp Leu Arg Ala Ala Ile Asn Asp Leu Gln Thr Val Val Val Gly Gly  
195 200 205

Tyr Glu Asp Ala Thr Gln Val Leu Ala Tyr Arg Asp Val Glu Lys Thr  
210 215 220

Val Phe Gln Ala Leu Gly Leu Val Phe Gly Ser Asp Asn Ala Lys Arg  
225 230 235 240

Ala Lys Met Ala Met Trp Asn Leu Asp Met Ser Pro Asp Glu Phe Leu  
245 250 255

Leu Trp Val Asp Glu Asn Ile Pro His Leu Tyr Leu Asn Pro Glu Glu  
260 265 270

Ile Ala Gln Ala Tyr Asp Ala Ile Ser Arg Ala Asp Ile Tyr Leu Gly  
275 280 285

Arg Ala Ala Arg Thr Gly Asn Tyr Ser Leu Trp Lys Tyr Ala Ile Asp  
290 295 300

Met Met Thr Ala Gly Val Ala Val Val Gly Arg Lys Arg Arg Gly Phe  
305 310 315 320

Val Lys Phe Tyr Pro Pro Asn Thr Leu Lys Ile Leu Ala Glu Ser Lys  
325 330 335

Glu Glu Arg Glu Ile Arg Glu Ser Ile Ile Lys Lys Ile Ile Arg Glu  
340 345 350

Met Xaa Met Ser Arg Leu Gln Ala Ile Glu Thr Met Lys Ile Ile Arg  
355 360 365

Glu Ile Phe Glu Asn Asn Leu Asp Leu Ala Ala His Phe Thr Val Phe  
370 375 380

Leu Gly Leu Ser Glu Lys Glu Val Glu Phe Leu Ala Gly Lys Glu Lys  
385 390 395 400

Ala Gly Thr Ile Trp Gly Lys Ala Leu Ala Leu Arg Arg Lys Leu Lys  
405 410 415

Glu Leu Gly Ile Arg Glu Glu Glu Lys Pro Lys Val Glu Ile Glu Glu  
420 425 430

Glu Glu Glu Glu Glu Lys Thr Glu Glu Lys Glu Glu Ile Glu  
435 440 445

Glu Lys Pro Glu Glu Glu Lys Glu Glu Lys Lys Glu Lys Glu Lys  
450 455 460

Pro Lys Lys Gly Lys Gln Ala Thr Leu Phe Asp Phe Leu Lys Lys  
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<211> 327  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
P38 clone

<400> 64

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20 25 30

Ile Val Lys Arg Leu Lys His Tyr Val Lys Thr Gly Ser Met Pro His  
35 40 45

Leu Leu Phe Ala Gly Pro Pro Gly Val Gly Lys Thr Thr Ala Ala Leu  
50 55 60

Ala Leu Ala Arg Glu Leu Phe Gly Glu Asn Trp Arg His Asn Phe Leu  
65 70 75 80

Glu Leu Asn Ala Ser Asp Glu Arg Gly Ile Asn Val Ile Arg Glu Lys  
85 90 95

Val Lys Glu Phe Ala Arg Thr Lys Pro Ile Gly Gly Ala Ser Phe Lys  
100 105 110

Ile Ile Phe Leu Asp Glu Ala Asp Ala Leu Thr Gln Asp Ala Gln Gln  
115 120 125

Ala Leu Arg Arg Thr Met Glu Met Phe Ser Ser Asn Val Arg Phe Ile  
130 135 140

Leu Ser Cys Asn Tyr Ser Ser Lys Ile Ile Glu Pro Ile Gln Ser Arg  
145 150 155 160

Cys Ala Ile Phe Arg Phe Arg Pro Leu Arg Asp Glu Asp Ile Ala Lys  
165 170 175

Arg Leu Arg Tyr Ile Ala Glu Asn Glu Gly Leu Glu Leu Thr Glu Glu  
180 185 190

Gly Leu Gln Ala Ile Leu Tyr Ile Ala Glu Gly Asp Met Arg Arg Ala  
195 200 205

Ile Asn Ile Leu Gln Ala Ala Ala Leu Asp Lys Lys Ile Thr Asp  
210 215 220

Glu Asn Val Phe Met Val Ala Ser Arg Ala Arg Pro Glu Asp Ile Arg  
225 230 235 240

Glu Met Met Leu Leu Ala Leu Lys Gly Asn Phe Leu Lys Ala Arg Glu  
245 250 255

Lys Leu Arg Glu Ile Leu Leu Lys Gln Gly Leu Ser Gly Glu Asp Val  
260 265 270

Leu Val Gln Met His Lys Glu Val Phe Asn Leu Pro Ile Glu Glu Pro  
275 280 285

Lys Lys Val Leu Leu Ala Asp Lys Ile Gly Glu Tyr Asn Phe Arg Leu  
290 295 300

Val Glu Gly Ala Asn Glu Ile Ile Gln Leu Glu Ala Leu Leu Ala Gln  
305 310 315 320

Phe Thr Leu Ile Gly Lys Lys  
325

<210> 65  
<211> 1077  
<212> DNA  
<213> Artificial Sequence

<220>  
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catgcagctg ctctcttact agcagaaagg ctgggaggtt aagttaccaa aagagaagaa 180  
caacctttaa tgaagattag cgaccatat ccaggaatgg atccccacga ggtcaacatt 240  
gttggaaagaa tacttaagaa gtatccaccg cgagaataaca caaagaagga tggaaagcatt 300  
ggaagggtt ccagtctagt tatatacgat gatactggga gagcgggggt tggctttgg 360  
gattcaaaag tttggagta ttacagcaag ctagaagtag gggatgttat taaggtttta 420  
gacgcccagg ttagggagag cttatctggt ttgcctgaat tgcacattaa cttcagggct 480  
agaataatta aaaacccaga tgatcttagg gttcaggata tcccacctct tgaagaagtt 540  
agagtggcaa ctatacgag aaagaagatc agtgaggctg agcctggggta tagatttgta 600  
gagcttaggg gaacaattgc caaagttac agatttttgg tatatgatgc atgtccagag 660  
tgttaagaaga agtttacta tgaccaggatggacgtttt ggtatgtcc agaacatgg 720  
gagggttggc caataaaaaat cactattttt gactttgggc ttgatgatgg ctcgggatac 780  
attaggatta ccctctttgg agacgtgtc gaagagttgc tgggagtagg gccagaagag 840  
attgccaaa agcttaagga aatggagagc atgggcatga ctctcaagga ggcagcggaga 900  
aaattggcgg agaagaggtt ctacaatata atagggaaag aaataatcg tggggaaat 960  
gtaatttggg acagggttctt gggcctaattc ttaagggcct cttctggga agaagttgac 1020  
tacaagagag aaatttggagag aatataagagg gaatttggaaag aatttgggggtt gatgtga 1077

<210> 66  
<211> 360  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Amino acid  
sequence of RFA clone

<400> 66  
Met Ile Met Ser Ala Phe Thr Lys Glu Glu Ile Ile Lys Arg Ile Leu  
1 5 10 15

Glu Glu Val Glu Gly Ile Thr Leu Glu Glu Ile Glu Asn Gln Ile Arg  
20 25 30

Gln Ile Met Arg Glu Asn Asn Ile Ser Glu His Ala Ala Ala Leu Leu  
35 40 45

Leu Ala Glu Arg Leu Gly Val Glu Val Thr Lys Arg Glu Glu Gln Pro  
50 55 60

Leu Met Lys Ile Ser Asp Leu Tyr Pro Gly Met Asp Pro His Glu Val  
65 70 75 80

Asn Ile Val Gly Arg Ile Leu Lys Lys Tyr Pro Pro Arg Glu Tyr Thr  
85 90 95

Lys Lys Asp Gly Ser Ile Gly Arg Val Ala Ser Leu Val Ile Tyr Asp  
100 105 110

Asp Thr Gly Arg Ala Arg Val Val Leu Trp Asp Ser Lys Val Leu Glu  
115 120 125

Tyr Tyr Ser Lys Leu Glu Val Gly Asp Val Ile Lys Val Leu Asp Ala  
130 135 140

Gln Val Arg Glu Ser Leu Ser Gly Leu Pro Glu Leu His Ile Asn Phe  
145 150 155 160

Arg Ala Arg Ile Ile Lys Asn Pro Asp Asp Pro Arg Val Gln Asp Ile  
165 170 175

Pro Pro Leu Glu Glu Val Arg Val Ala Thr Tyr Thr Arg Lys Lys Ile  
180 185 190

Ser Glu Val Glu Pro Gly Asp Arg Phe Val Glu Leu Arg Gly Thr Ile  
195 200 205

Ala Lys Val Tyr Arg Val Leu Val Tyr Asp Ala Cys Pro Glu Cys Lys  
210 215 220

Lys Lys Val Asp Tyr Asp Pro Gly Met Asp Val Trp Ile Cys Pro Glu  
225 230 235 240

His Gly Glu Val Glu Pro Ile Lys Ile Thr Ile Leu Asp Phe Gly Leu  
245 250 255

Asp Asp Gly Ser Gly Tyr Ile Arg Ile Thr Leu Phe Gly Asp Asp Ala  
260 265 270

Glu Glu Leu Leu Gly Val Gly Pro Glu Glu Ile Ala Gln Lys Leu Lys  
275 280 285

Glu Met Glu Ser Met Gly Met Thr Leu Lys Glu Ala Ala Arg Lys Leu  
290 295 300

Ala Glu Glu Glu Phe Tyr Asn Ile Ile Gly Lys Glu Ile Ile Val Arg  
305 310 315 320

Gly Asn Val Ile Glu Asp Arg Phe Leu Gly Leu Ile Leu Arg Ala Ser  
325 330 335

Ser Trp Glu Glu Val Asp Tyr Lys Arg Glu Ile Glu Arg Ile Lys Arg  
340 345 350

Glu Leu Glu Glu Leu Gly Val Met  
355 360

<210> 67  
<211> 2604  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant helicase 2

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aagaggctcg gatttagact ttattctcac caagttaaag ccctagaaaa gctgtattca 180  
gggaaaaacg tagttgttc aacgcccaca gcttagtggaa aaagcgagat atttaggtt 240  
tttatcttg acgaaatact gtcaagcccg tcctcaactt ttctcttaat ctacccaaca 300  
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atttgtggaa aaagagttcg agcagaagtc ttaactggag atacggaatg ggaaaagaga 420  
agagaatca ttaggagcaa accaaacgta atcttcacga caccgataat gcttcatcat 480  
cacattcttc ccaggtggag ggattatttc tggctttaa aggggcttag acttcctgtc 540  
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ctcggttggagg gaatagaaaaa gggcttagt gagaatggatcc ccgttaactt ggacaatgaa 1260  
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gaaattggagg ggagatggaa gagattcata aagaccctcg tagaggaggg atacgtggaa 1380  
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<210> 68

<211> 2511

**<212> DNA**

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant helicase 3

<400> 68

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ataatgagag ataataagact ttttaaagct cttgaaggaa gtcagtattt aaatccaaag 180  
gaagtggaga gagcccttag aaattcaagg atagttctgg tgaatgccaa cgagtggaa 240  
gagtactta agaagaggtt aatgaacaaa agagttaaa aagctgacat ctgtaggctc 300  
tgccttctca atggaaagat tacagtaactc actgagggaa acaggataag atacagagat 360  
gaatacatat gtgaaagttg tgccgaggag gagttgaaga gagagttaag atttcgattt 420  
aattccatag gaatgcttga acagccaaag aagcttttag agagattcag agatttagac 480  
aaggtgattt caatttttga tccatcctt gaccccacta agcatccaga gataacaaa 540  
tggatgagc taaaggccaa gcatataagg gtcgagaaga tgcatataga tgagctaac 600  
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tggataacag ttagggagtt tcaccaaattt cttggcaggg ctggaaaggcc acagtaccat 1620  
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gcaattgaaa gaatagcccc agtgttcaat aagagaagag tggtagaaga cacaatcagg 2460  
gttagaaaggg aaattgaaga aggaaaaattt ttgaagggtt agagacgtat a 2511

<210> 69  
<211> 2943  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant helicase 4

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cctttcttat acatacaatg ttttcttat ctacctctt taaaactttt aaactccttg 180  
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ttgaatgccc ttcaacaattt agcctttcat aaaatttaggg gagaaggtaa aagtgtttt 300  
ataatagctc cgacaggaag cggaaaaactt gaagccgcag taattccat cttagacgca 360  
atactacggg agaatctttaa acctatagca gctatttata tagccccattt gaaggcacta 420  
aataggact tgcctagagag actaaagtgg tggaaagaaaa aaactggggt aataatagag 480

<210> 70  
<211> 2295  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant helicase 5

<400> 70

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gctatgtga tagcagagta tagattaacg aaatatggcg gaaaagttct aatgctcgcc 180
cccactaagc ctctcggtct tcaacatgcg gaaagttta ggaggctatt taacctccct 240
ccagaaaaaa ttgttagcact tactggagag aagagcccg aagagagaag taaggcctgg 300
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agaatatctt tagaagacgt ttcqctaata qtattcqatq aaqctcacaaq aqctqtcqcc 420

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<210> 71  
<211> 2823  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant  
helicase 6

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aaaatttaca aaccattttc ccagataga agatattcg tggtaagaa tggggaaagat 2760  
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<210> 72  
<211> 3837

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant helicase 7

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ataacagaca caataatcg aatttcagcc ttgttaaaga ataggcaaaa tggagagcgg 1200  
ataattgtta agtcgtcg tgagcccccc atagaagttt cagatgccca agaaaaggag 1260  
agaatgttc taattgagtt cttagggat gttattgtat ccgtaaagtc actatctcca 1320  
accgataaaag tctacctaca catgtacttt tacaatagaa aacagagaga tgaccttatg 1380  
gatgccgtaa agagacacaa agagataaga gaaaacaatg cagtcgtggc cttgctaagc 1440  
ttgagaagag ccatagattt ggagagctt tcaataataa aggtatgagat aataaggagg 1500  
catgccttac cactttctcc tggctggta ttcttacag ttgtactca gtttggatac 1560  
agatggagaa ggaacaaaaac ctttgcgcga atgcttgagg ttgttagcaag aagagaaaat 1620  
ggttaagataa atctcaaaaac tctccttaac atttctgaaa cgggaatttg gccagaatat 1680  
tatccaatca tcgataggga taacgaagga atacccttca cactttctg gagcgcactg 1740  
gtcaaattag ctactgagga agacaattca agaattaaga gggatataag ggacataactc 1800  
tcccaaattgg ttgaggccct caaaacattt gaagagagaa ttcccggca atataaagac 1860  
gccttcgtga aaaaagaggg aataacccaa gaagatctcg aaaacttga cataaagaag 1920  
gaagaattag ctgatattcc tcttgaatac ttacaattag agttcgatgc aagatttaga 1980  
gaacgatccg aatactatacg gcttccccta tcaataagag catactcaga ggaatcagca 2040  
ctaattaaga tagaaaaacat tgaaaagaag aaaaatgact gtctgttgc tggaaaaatc 2100  
gtgctaattt acgaaaaatgg aagaataaaa gagtataatc caaaagaagt tcttatacgat 2160  
attgatgaag gtctctttgt agttgttaacg ccaaagaaaat tcttagataa gctaagaaga 2220  
gatcccggttc aaagaataag caaatcaccg ttaggaatag ttgaggctat agatcaccg 2280  
acaggaaaaag ttgttataag gttataaga gtctctcccg gcagatttac actcaaacac 2340  
tctaaggtaa ttgttaaaaa tggactattt acaataaccc ttcctgaagg ggaagtgaaa 2400  
gttactctcg gagagatagt tatagtagat cctagcgtcg atgacatagg aatggaaagg 2460  
gcatacaatg tgctctcaga aatatccaa ggggaactca agcatgaaat ttatcagaag 2520  
gtcaaagcaa tatacgaagg gaacacggaa tcaagatacg aagtcaacat ctggaaagaaa 2580  
aagcacatag aagaatttc ctccagagtt aagaagatca acgaaagaaca gaaaaatgtt 2640  
gcaatttgcataaacaactt tctagtcacc cttcaaggcc cccctggac tggaaagaca 2700  
tcagggccca tagccccacg aatttcgcac agagcatatt caatggtcaa ggacaaaaag 2760  
aatggcctct ttgttagttac tggagtctca cacagggcag ttaatgaggc cctgataaag 2820  
actttaaagc taaagaaaaga gctggagaat acattaaaag agcttagaaa gatagatcta 2880  
attagagcag tctctgggg aagggcaatc aaaataatta aagaggaact agagaggaa 2940  
ataaaggatg atgtcgacag aatttagattt acagcacaag aaatttaccc ctcttcaaag 3000  
caaagatcat tagacaataa ttttgcata tctggaaactg tgaggatagt atttggaaaca 3060  
ccacagactt tgaacacaagct tatgaagaat acaaaaagaag tcgaactagt tgtcatagat 3120  
gaagcttagta tgatggactt accaatgttc ttctctcaa caaaagttt taaaggtaaa 3180  
gttctcttgg tcggggatca cagggagatg gagccaattc aagtcgtat atggcaatta 3240  
gaggacagaa agacatttga agagcactat ccattccctt cagcccttaa cttcattaga 3300  
tttctcaggg gagagttgg tggaaagagaa ctttggaaatg ttaagagaat ctttggagg 3360  
gaacctccag aatggaaagaa ggacaagaac gaggttctcc ctctctatag gttagtaaga 3420  
acttataatgt tgccccaggg aatagctgtat ctactgagtg atgcaatata cagagcagat 3480  
ggcataaaat tgattagtga aaagaaaaag aggagaaaaga taattggcag gcacaaaggat 3540  
gagtttctat cgatagttt agatgacagg ttttttttcg ttcttaatact tcgtacgag 3600  
ggcaatttcca caaagattaa cgagctggaa gcaaagatag tagagaagat aatcaaaaaga 3660  
gttagagaata ttgtatatagg agttgttagt ccatatagag ctccaaaagag attaataatgt 3720  
tcattaaatag atagtgcaca ggtggacaca gttgagatg tccaaagggggg agagaaaatct 3780  
ttaatagtaa ttcaatgac ttccagcgac ccccgatatac ctggaaagg ttttgcatac 3837

<210> 73  
<211> 1968  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant  
helicase dna2

<400> 73  
atgaacataa agagcttcat aaacaggctt aaggagctag ttgaaatcg gaggaaagct 60  
gaaatagagg ctatgaggtt ggagatgaaa aggcttagcg gagtgagag ggagaggtta 120  
ggtagggcaa ttctcagttt aaacggtaaa atcgttggtg aagagctcg ttatattcttgc 180

gttaagtacg gaaggaataa ggagataaag accgagatca gcgttggga tttggttgtt 240  
ataagcaaga gggatcccct gaagagcgcac ctcctggaa ctgttgtga gaaggggaag 300  
agattcatcg tcgttgcctt agaaccagtc ccagagtggg cccttagaga tgtgaggata 360  
gacctctacg ccaacgataat aacattcaag aggtggatcg aaaacctcg aagggtttagg 420  
aaggctggaa aaaaggctt agagtttac ttaggtttag atgagccttc ccagggggag 480  
gaagttagct ttaaaccctt tgataagagc ctaaaccctt ctcaaaggaa agcgatagct 540  
aaggcttag gtatgtaaaga cttcttcctt atccacggcc cctttggaa tggaaagacg 600  
aggacttag tttagctgat tagcaggag gtaaaagaggg ggaacaaaagt tctagctaca 660  
gctgagagca acgttgcgt ggacaattt aatggaaagat tggccaaaga tggagttaaag 720  
atagtttaggg ttgggcaccc aagttaggtt tcgaggcatt tgcacgagac aactttagct 780  
tacctcatta ctcagcacga gctctacggt gagcttaggg agcttaggtt gatagggcag 840  
agtttggcag agaagaggga cacatataca aagccgactc caaagttcag gaggggactg 900  
agtgtatctg agataattaa gttggccgag aagggaaagag gggctagagg actctcagct 960  
agactaataa aggagatggc cgagtggata aagctaaaca ggcaggttca gaaggccctt 1020  
gaagatgcta gaaagcttga ggagaggatt gcgagggata taatttaggg agccgatgtg 1080  
gttttgcacaa ctaactcttc tgcagccctt gatgttggat atgctaccga ttatgtatgtt 1140  
gcgataataag atgaagcaac tcaggcaact ataccgagca tattaatacc tctcaacaag 1200  
gttgataggt ttataacttgc tggagaccac aagcaactac caccaactat cttaaagcttg 1260  
gaggccagg agctctccca cacgttttc gagggtttaa ttgagaagta cccatgaaag 1320  
agcgaaatgc tgacaattca gtataggatg aatgagagga taatggagtt tccgagcagg 1380  
gagtttacg atgaaagaat agttgtgtat gaaagtgtaa aaaacataac tctggccgac 1440  
ctgggaatta aagttaatgc tagtggata tggagggaca tccttagatcc aaacaacgtc 1500  
ctcgtttca tagatacttg catgctcgaa aataggttgc agaggcagag aaggggaaagc 1560  
gaaagcaggg agaattccctt ggaggccaag atagtggacaa aatcggttca aaagctttg 1620  
gaaagtgggg ttaaagcgga aatgatggga gtgattacac cttacgatga ccagaggat 1680  
ttgataagct tgaatgttcc cgaagaagtt gaggtcaaga ctgtggatgg ttaccaggaa 1740  
agggagaagg aagtgataat tctatcattt gtccgctcta acaaagcggg agagatccgc 1800  
tttctcaagg acttggaggag gctaaacgtg tccttaacta gggctaaagag gaagcttatac 1860  
atgattggcg attcctcaac gcttcatct cacgaaacct acaggaggtt aatcgagcac 1920  
tgagggaga aggggttata tggatgtctt acgaaggata gcatttga 1968

<210> 74  
<211> 867  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Helicase 2

<400> 74  
Met Ile Glu Glu Leu Phe Lys Gly Leu Glu Ser Glu Ile Val Gly Leu  
1 5 10 15

His Glu Ile Pro Pro Lys Arg Gly Glu Tyr Gly Glu Phe Lys Phe Arg  
20 25 30

Asn Glu Glu Val Asn Glu Leu Val Lys Arg Leu Gly Phe Arg Leu Tyr  
35 40 45

Ser His Gln Val Lys Ala Leu Glu Lys Leu Tyr Ser Gly Lys Asn Val  
50 55 60

Val Val Ser Thr Pro Thr Ala Ser Gly Lys Ser Glu Ile Phe Arg Leu  
65 70 75 80

Phe Ile Phe Asp Glu Ile Leu Ser Ser Pro Ser Ser Thr Phe Leu. Leu  
85 90 95

Ile Tyr Pro Thr Arg Ala Leu Ile Asn Asn Gln Met Glu Lys Phe Glu  
100 105 110

Lys Glu Asn Thr Ile Phe Glu Glu Ile Cys Gly Lys Arg Val Arg Ala  
115 120 125

Glu Val Leu Thr Gly Asp Thr Glu Trp Glu Lys Arg Arg Glu Ile Ile  
130 135 140

Arg Ser Lys Pro Asn Val Ile Phe Thr Thr Pro Asp Met Leu His His  
145 150 155 160

His Ile Leu Pro Arg Trp Arg Asp Tyr Phe Trp Leu Leu Lys Gly Leu  
165 170 175

Arg Leu Leu Val Val Asp Glu Leu His Val Tyr Arg Gly Ile Phe Gly  
180 185 190

Thr Asn Val Ala Tyr Val Phe Lys Arg Leu Phe Leu Arg Leu Lys Arg  
195 200 205

Leu Ser Ser Ser Pro Gln Ile Leu Ala Leu Ser Ala Thr Leu Arg Asn  
210 215 220

Pro Lys Glu Phe Ala Glu Gln Phe Phe Glu Thr Glu Phe Glu Glu Val  
225 230 235 240

Lys Glu Ala Gly Ser Pro Ser Pro Arg Arg Ile Ile Val Met Phe Glu  
245 250 255

Pro Arg Arg Phe Thr Gly Glu Gln Leu Ile Lys Gln Ile Val Glu Arg  
260 265 270

Leu Thr Arg Lys Asn Ile Lys Thr Leu Val Phe Phe Asp Ser Arg Lys  
275 280 285

Gly Thr Glu Arg Ile Met Arg Leu Phe Leu Phe Ser Asp Ala Phe Asp  
290 295 300

Arg Ile Thr Thr Tyr Lys Gly Thr Leu Thr Lys Arg Glu Arg Phe Leu  
305 310 315 320

Ile Glu Arg Asp Phe Arg Glu Gly Asn Leu Thr Val Leu Leu Thr Thr  
325 330 335

Asn Ala Leu Glu Leu Gly Ile Asp Ile Gly Asp Leu Asp Ala Val Ile  
340 345 350

Asn Tyr Gly Ile Pro Ser Asp Gly Leu Phe Ser Leu Ile Gln Arg Phe  
355 360 365

Gly Arg Ala Gly Arg Asp Pro Asn Arg Ile Ala Ile Asn Gly Ile Ile  
370 375 380

Leu Arg Arg Asn Gly Leu Asp Tyr Tyr Lys Glu His Phe Asp Glu  
385 390 395 400

Leu Val Glu Gly Ile Glu Lys Gly Leu Val Glu Lys Ile Pro Val Asn  
405 410 415

Leu Asp Asn Glu Lys Ile Ala Lys Lys His Leu His Tyr Ala Ile Ala  
420 425 430

Glu Leu Gly Val Val Ser Ile Lys Glu Ile Glu Gly Arg Trp Lys Arg  
435 440 445

Phe Ile Lys Thr Leu Val Glu Glu Gly Tyr Val Glu Val Thr Arg Asn  
450 455 460

Pro Ile Thr Gly Glu Glu Ile Arg Leu Arg Arg Pro Pro Val Tyr  
465 470 475 480

Ser Ser Ile Arg Thr Ala Ser Asp Glu Ser Tyr Phe Leu Val Val Asp  
485 490 495

Glu Pro Trp Ile Arg Gly Ala Leu Gln Arg Lys Arg Gly Ala Glu Leu  
500 505 510

Leu Arg Phe Val Asn Tyr Leu Lys Val Arg Gly Met Val Val Glu Glu  
515 520 525

Val Asp Glu Ile Glu Phe His Arg Ser Leu Leu Pro Gly Met Val Tyr  
530 535 540

Leu Ser Arg Gly Arg Pro Tyr Met Ala Val Asp Lys Ile Lys Ile Glu  
545 550 555 560

Lys Phe His Phe Val Phe Ala Arg Pro Leu Pro Ile Glu Glu Ile  
565 570 575

Asp Thr Ser Ser Lys Ile Glu Asn Ile Glu Ile Leu Glu Val Lys  
580 585 590

Asp Glu Lys Thr Val Gly Pro Ile Lys Val Lys Phe Gly Arg Leu Arg  
595 600 605

Val Arg His Glu Tyr Thr Gly Tyr Ala Val Arg Gly Arg Asp Val Glu  
610 615 620

Arg His Val Lys Arg Leu Glu Glu Leu Lys Asp Glu Gly Ile Leu Arg  
625 630 635 640

Gly Glu Ile Asp Ile Val Pro Tyr Ile Trp Glu Ser Trp Lys Phe Ala  
645 650 655

Arg Val Leu Phe Asp Thr Pro Tyr Ile Arg Glu Phe Glu Thr Glu Gly  
660 665 670

Phe Trp Leu Glu Phe Pro Asn Asp Ile Arg Ile Val Pro Glu Glu Glu  
675 680 685

Phe Arg Glu Phe Phe Ala Val Ala Ser Glu Ile Asp Pro Glu Leu Ala  
690 695 700

Met Phe Leu Tyr Asn Arg Ile Ser Arg Lys Ser Leu Phe Pro Thr Leu  
705 710 715 720

Leu Gly Ala Thr Thr His Tyr Ile Arg Ser Phe Ile Leu His His Ala  
725 730 735

Lys Asp Lys Gly Glu Glu Phe Ala Phe Ala Val Lys Lys Met Ile Asp  
740 745 750

Ser Lys Asp Gly Ile Gly Ser Gly Leu His Ala Ile Glu Pro Asn Ile

755

760

765

Ile Lys Leu Ala Pro Val Val Thr His Val Asp Ser Arg Glu Ile Gly  
770 775 780

Gly Tyr Ser Tyr Asp Asp Phe His Gly Lys Pro Val Ile Phe Ile Tyr  
785 790 795 800

Asp Gly Asn Glu Gly Gly Ser Gly Ile Ile Arg Gln Val Tyr Glu Asn  
805 810 815

Val Glu Lys Leu Met Tyr Arg Ser Leu Glu His Ile Lys Lys Cys Pro  
820 825 830

Cys Lys Asp Gly Cys Pro Ala Cys Ile Tyr Ser Pro Lys Cys Gly Thr  
835 840 845

Phe Asn Glu Phe Leu Asp Lys Trp Met Ala Ile Arg Ile Trp Glu Lys  
850 855 860

Val Leu Pro  
865

<210> 75

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Helicase 3

<400> 75

Met Leu Ile Val Val Arg Pro Gly Arg Lys Lys Asn Glu Leu Glu Ala  
1 5 10 15

Phe Ile Ile Glu Asn Pro Pro Glu Lys Leu Ser Gln Arg Arg Asn Leu  
20 25 30

Lys Ala Asp Arg Val Val Arg Leu Ile Met Arg Asp Asn Arg Leu Phe  
35 40 45

Lys Ala Leu Glu Gly Ser Gln Tyr Leu Asn Pro Lys Glu Val Glu Arg  
50 55 60

Ala Leu Arg Asn Ser Arg Ile Val Leu Val Asn Ala Asn Glu Trp Glu  
65 70 75 80

Glu Tyr Phe Lys Lys Arg Leu Met Asn Lys Arg Val Glu Lys Ala Asp  
85 90 95

Ile Cys Arg Leu Cys Leu Leu Asn Gly Lys Ile Thr Val Leu Thr Glu  
100 105 110

Gly Asn Arg Ile Arg Tyr Arg Asp Glu Tyr Ile Cys Glu Ser Cys Ala  
115 120 125

Glu Glu Glu Leu Lys Arg Glu Leu Arg Phe Arg Phe Asn Ser Ile Gly  
130 135 140

Met Leu Glu Gln Ala Lys Lys Leu Leu Glu Arg Phe Arg Asp Leu Asp

145 150 155 160  
Lys Val Ile Ser Ile Phe Asp Pro Ser Phe Asp Pro Thr Lys His Pro  
165 170 175  
Glu Ile Thr Lys Trp Asp Glu Leu Lys Ala Lys His Ile Arg Val Glu  
180 185 190  
Lys Met His Ile Asp Glu Leu Asn Ile Pro Glu Glu Phe Lys Lys Val  
195 200 205  
Leu Lys Ala Glu Gly Ile Asn Glu Leu Leu Pro Val Gln Val Leu Ala  
210 215 220  
Ile Lys Asn Gly Leu Leu Glu Gly Glu Asn Leu Leu Val Val Ser Ala  
225 230 235 240  
Thr Ala Ser Gly Lys Thr Leu Ile Gly Glu Leu Ala Gly Ile Pro Lys  
245 250 255  
Ala Leu Lys Gly Lys Lys Met Leu Phe Leu Val Pro Leu Val Ala Leu  
260 265 270  
Ala Asn Gln Lys Tyr Glu Asp Phe Lys Arg Arg Tyr Ser Lys Leu Gly  
275 280 285  
Leu Lys Val Ala Ile Arg Val Gly Met Ser Arg Ile Lys Thr Lys Glu  
290 295 300  
Glu Pro Ile Val Leu Asp Thr Gly Thr Asp Ala His Ile Ile Val Gly  
305 310 315 320  
Thr Tyr Glu Gly Ile Asp Tyr Leu Leu Arg Ala Gly Lys Lys Ile Gly  
325 330 335  
Asn Val Gly Thr Val Val Ile Asp Glu Ile His Met Leu Asp Asp Glu  
340 345 350  
Glu Arg Gly Ala Arg Leu Asp Gly Leu Ile Ala Arg Leu Arg Lys Leu  
355 360 365  
Tyr Ser Asn Ala Gln Phe Ile Gly Leu Ser Ala Thr Val Gly Asn Pro  
370 375 380  
Gln Glu Leu Ala Arg Lys Leu Gly Met Lys Leu Val Leu Tyr Asp Glu  
385 390 395 400  
Arg Pro Val Asp Leu Glu Arg His Leu Ile Ile Ala Arg Asn Glu Ser  
405 410 415  
Glu Lys Trp Arg Tyr Ile Ala Lys Leu Cys Lys Ala Glu Ala Met Arg  
420 425 430  
Lys Ser Glu Lys Gly Phe Lys Gly Gln Thr Ile Val Phe Thr Phe Ser  
435 440 445  
Arg Arg Arg Cys His Glu Leu Ala Ser Phe Leu Thr Gly Gln Gly Leu  
450 455 460  
Lys Ala Lys Ala Tyr His Ser Gly Leu Pro Tyr Val Gln Arg Lys Leu  
465 470 475 480

Thr Glu Met Glu Phe Gln Ala Gln Met Ile Asp Val Val Val Thr Thr  
485 490 495

Ala Ala Leu Gly Ala Gly Val Asp Phe Pro Ala Ser Gln Val Ile Phe  
500 505 510

Glu Ser Leu Ala Met Gly Asn Lys Trp Ile Thr Val Arg Glu Phe His  
515 520 525

Gln Met Leu Gly Arg Ala Gly Arg Pro Gln Tyr His Glu Lys Gly Lys  
530 535 540

Val Tyr Ile Ile Val Glu Pro Gly Lys Lys Tyr Ser Ala Gln Met Glu  
545 550 555 560

Gly Thr Glu Asp Glu Val Ala Leu Lys Leu Leu Thr Ser Pro Ile Glu  
565 570 575

Pro Val Ile Val Glu Trp Ser Asp Glu Phe Glu Glu Asp Asn Val Leu  
580 585 590

Ala His Ala Cys Val Phe Asn Arg Leu Lys Val Ile Glu Glu Val Gln  
595 600 605

Ser Leu Cys Leu Gly Ala Asn Gln Ser Ala Lys Asn Val Leu Glu Lys  
610 615 620

Leu Met Glu Lys Gly Leu Val Lys Ile Tyr Gly Asp Lys Val Glu Ala  
625 630 635 640

Thr Pro Tyr Gly Arg Ala Val Ser Met Ser Phe Leu Leu Pro Arg Glu  
645 650 655

Ala Glu Phe Ile Arg Asp Asn Leu Glu Ser Thr Asp Pro Ile Glu Ile  
660 665 670

Ala Ile Lys Leu Leu Pro Phe Glu Asn Val Tyr Leu Pro Gly Ser Leu  
675 680 685

Gln Arg Glu Ile Glu Ser Ala Val Arg Gly Lys Ile Ser Ser Asn Ile  
690 695 700

Phe Ser Ser Ser Phe Ala Ser Val Leu Glu Leu Asp Lys Ile Ile  
705 710 715 720

Pro Glu Ile Ser Pro Asn Ala Ala Glu Arg Leu Phe Leu Ile Tyr Gln  
725 730 735

Asp Phe Phe Asn Cys Pro Glu Gln Asp Cys Thr Glu Phe Ala Met Glu  
740 745 750

Arg Ile Gly Arg Lys Ile Ile Asp Leu Arg Arg Glu Gly Tyr Glu Pro  
755 760 765

Ser Lys Ile Ser Glu His Phe Arg Lys Val Tyr Ala Leu Ile Leu Tyr  
770 775 780

Pro Gly Asp Val Phe Thr Trp Leu Asp Gly Ile Val Arg Lys Leu Glu  
785 790 795 800

Ala Ile Glu Arg Ile Ala Arg Val Phe Asn Lys Arg Arg Val Val Glu  
805 810 815

Asp Thr Ile Arg Val Arg Arg Glu Ile Glu Glu Gly Lys Ile Leu Lys  
820 825 830

Gly Glu Arg Arg  
835

<210> 76  
<211> 980  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Helicase 4

<400> 76  
Met His Lys Tyr Phe Phe Pro Leu Pro Ala Thr Lys Ser Thr Phe Leu  
1 5 10 15

Leu Pro Ala Asp Leu Thr Thr Ala Asn Pro Cys Phe Ser Lys Ser Leu  
20 25 30

Ile Asn Ser Leu Ser Ala Trp Ala Pro Phe Leu Tyr Ile Gln Cys Phe  
35 40 45

Ser Tyr Leu Pro Leu Ile Asn Phe Leu Asn Ser Leu Thr Tyr Pro Leu  
50 55 60

Glu Met His Ile Leu Ile Lys Lys Ala Ile Lys Glu Arg Phe Gly Lys  
65 70 75 80

Leu Asn Ala Leu Gln Gln Leu Ala Phe His Lys Ile Arg Gly Glu Gly  
85 90 95

Lys Ser Val Leu Ile Ile Ala Pro Thr Gly Ser Gly Lys Thr Glu Ala  
100 105 110

Ala Val Ile Pro Ile Leu Asp Ala Ile Leu Arg Glu Asn Leu Lys Pro  
115 120 125

Ile Ala Ala Ile Tyr Ile Ala Pro Leu Lys Ala Leu Asn Arg Asp Leu  
130 135 140

Leu Glu Arg Leu Lys Trp Trp Glu Glu Lys Thr Gly Val Ile Ile Glu  
145 150 155 160

Val Arg His Gly Asp Thr Pro Thr Ser Lys Arg Leu Lys Gln Val Lys  
165 170 175

Asn Pro Pro His Leu Leu Ile Thr Thr Pro Glu Met Leu Pro Ala Ile  
180 185 190

Leu Thr Thr Lys Ser Phe Arg Pro Tyr Leu Lys Asn Thr Lys Phe Ile  
195 200 205

Val Ile Asp Glu Ile Gly Glu Leu Ile Glu Asn Lys Arg Gly Thr Gln  
210 215 220

Leu Ile Leu Asn Leu Lys Arg Leu Glu Leu Ile Thr Glu Asp Lys Pro  
225 230 235 240

Ile Arg Ile Gly Leu Ser Ala Thr Ile Gly Ser Glu Glu Lys Val Arg  
245 250 255

Leu Trp Met Glu Ala Asp Glu Val Val Lys Pro Arg Leu Lys Lys Lys  
260 265 270

Tyr Lys Phe Thr Val Leu Tyr Pro Gln Pro Ile Pro Glu Asp Glu Lys  
275 280 285

Leu Ala Glu Glu Leu Lys Val Pro Ile Glu Val Ala Thr Arg Leu Arg  
290 295 300

Val Val Trp Asp Ile Val Glu Lys His Lys Lys Val Leu Ile Phe Val  
305 310 315 320

Asn Thr Arg Gln Phe Ala Glu Ile Leu Gly His Arg Leu Lys Ala Trp  
325 330 335

Gly Lys Pro Val Glu Val His His Gly Ser Leu Ser Arg Glu Ala Arg  
340 345 350

Ile Glu Ala Glu Lys Lys Leu Lys Glu Gly Lys Ile Lys Ala Leu Ile  
355 360 365

Cys Thr Ser Ser Met Glu Leu Gly Ile Asp Ile Gly Asp Val Asp Ala  
370 375 380

Val Ile Gln Tyr Met Ser Pro Arg Gln Val Asn Arg Leu Val Gln Arg  
385 390 395 400

Ala Gly Arg Ser Lys His Arg Leu Trp Glu Thr Ser Glu Ala Tyr Ile  
405 410 415

Ile Thr Thr Asn Val Glu Asp Tyr Leu Gln Ser Leu Ala Ile Ala Lys  
420 425 430

Leu Ala Leu Glu Gly Lys Leu Glu Asp Val Asn Pro Tyr Glu Asn Ala  
435 440 445

Leu Asp Val Leu Ala His Phe Ile Val Glu Leu Thr Ile Glu Tyr Arg  
450 455 460

Asn Val Asn Ile Thr Glu Pro Tyr Ser Leu Ala Lys Ser Thr Tyr Pro  
465 470 475 480

Tyr Arg Lys Leu Ser Trp Glu Asp Tyr Gln Lys Val Leu Glu Ile Leu  
485 490 495

Glu Glu Ala Arg Ile Ile Arg Arg Asp Gly Asp Ala Ile Lys Leu Gly  
500 505 510

Lys Asn Ala Phe Lys Tyr Tyr Phe Glu Asn Leu Ser Thr Ile Pro Asp  
515 520 525

Glu Ile Ser Tyr Ala Val Ile Asp Ile Ala Ser Gly Lys Ser Val Gly  
530 535 540

Arg Leu Asp Glu Asn Phe Val Thr Glu Leu Glu Glu Ser Met Glu Phe

545	550	555	560
Ile Met His Gly Arg Ser Trp Ile Val Leu Glu Ile Asn Glu Lys Glu			
565	570	575	
Arg Ile Ile Lys Val Lys Glu Ser Asn Asn Leu Glu Ser Ala Leu Pro			
580	585	590	
Ser Trp Glu Gly Glu Leu Ile Pro Val Pro Leu Glu Val Ala Glu Phe			
595	600	605	
Val Gly Lys Leu Lys Arg Glu Leu Leu Trp Asp Lys Glu Arg Ala Leu			
610	615	620	
Lys Leu Leu Glu Gly Val Glu Phe Asn Lys Glu Glu Leu Glu Val Ala			
625	630	635	640
Ile Ser Gln Leu Val Glu Ser Glu Pro Val Ala Ser Asp Arg Asp Ile			
645	650	655	
Ile Ile Glu Ser Tyr Pro Lys Phe Val Ile Ile His Ala Asp Phe Gly			
660	665	670	
Asn Lys Ile Asn Glu Gly Leu Thr Arg Phe Ile Ser Val Phe Leu Ser			
675	680	685	
Ala Arg Tyr Gly Asn Ile Phe Leu Pro Arg Ser Gln Ala His Gly Ile			
690	695	700	
Ile Ile Arg Ser Pro Phe Arg Leu Asn Pro Glu Glu Ile Lys Glu Ile			
705	710	715	720
Leu Leu Met Lys Ala Glu Val Gly Asp Ile Val Ala Arg Gly Ile Arg			
725	730	735	
Asp Thr Pro Ile Tyr Arg Trp Lys Met Ser Ala Ile Ala Lys Arg Phe			
740	745	750	
Gly Ala Leu Arg Arg Asp Ala Arg Ile Lys Lys Val Glu Arg Leu Phe			
755	760	765	
Glu Gly Thr Ile Ile Glu Lys Glu Thr Phe Asn Glu Ile Tyr His Asp			
770	775	780	
Lys Ile Asp Ile Asp Lys Thr Glu Lys Ile Leu Glu Lys Ile Arg Lys			
785	790	795	800
Gly Glu Ile Arg Met Lys Thr Leu Phe Arg Glu Glu Ile Thr Pro Leu			
805	810	815	
Ser Ser Ser Leu Ala Thr Leu Gly Gly Glu Phe Leu Ile Arg Asp Ile			
820	825	830	
Leu Thr Gln Glu Glu Val Glu Glu Ile Phe Arg Glu Lys Leu Leu Asp			
835	840	845	
Ala Glu Leu Val Met Val Cys Thr Asn Cys Gly Phe Ser Trp Arg Thr			
850	855	860	
Lys Val Arg Arg Val Met Asp Arg Val Asn Glu Leu Ser Cys Pro Lys			
865	870	875	880

Cys Asp Ser Lys Met Ile Ala Pro Leu His Pro Lys Asp Ser Glu Thr  
885 890 895  
Phe Ile Ser Ala Leu Lys Lys Leu Lys Arg Gly Glu Lys Leu Ser Arg  
900 905 910  
Glu Glu Glu Lys Tyr Tyr Leu Arg Gly Leu Lys Ala Ala Asp Leu Leu  
915 920 925  
Lys Ala Tyr Gly Lys Asp Ala Leu Leu Ala Leu Ala Thr Tyr Gly Val  
930 935 940  
Gly Val Glu Ser Ala Thr Arg Ile Leu Arg Asp Tyr Arg Gly Lys Ser  
945 950 955 960  
Leu Ile Lys Ala Leu Ile Glu Ala Glu Lys His Tyr Ile Gln Thr Arg  
965 970 975  
Lys Phe Trp Glu  
980

<210> 77  
<211> 764  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Helicase 5

<400> 77  
Val Met Leu Leu Arg Arg Asp Leu Ile Gln Pro Arg Ile Tyr Gln Glu  
1 5 10 15

Val Ile Tyr Ala Lys Cys Lys Glu Thr Asn Cys Leu Ile Val Leu Pro  
20 25 30

Thr Gly Leu Gly Lys Thr Leu Ile Ala Met Met Ile Ala Glu Tyr Arg  
35 40 45

Leu Thr Lys Tyr Gly Gly Lys Val Leu Met Leu Ala Pro Thr Lys Pro  
50 55 60

Leu Val Leu Gln His Ala Glu Ser Phe Arg Arg Leu Phe Asn Leu Pro  
65 70 75 80

Pro Glu Lys Ile Val Ala Leu Thr Gly Glu Lys Ser Pro Glu Glu Arg  
85 90 95

Ser Lys Ala Trp Ala Arg Ala Lys Val Ile Val Ala Thr Pro Gln Thr  
100 105 110

Ile Glu Asn Asp Leu Leu Ala Gly Arg Ile Ser Leu Glu Asp Val Ser  
115 120 125

Leu Ile Val Phe Asp Glu Ala His Arg Ala Val Gly Asn Tyr Ala Tyr  
130 135 140

Val Phe Ile Ala Arg Glu Tyr Lys Arg Gln Ala Lys Asn Pro Leu Val  
145 150 155 160

Ile Gly Leu Thr Ala Ser Pro Gly Ser Thr Pro Glu Lys Ile Met Glu  
165 170 175

Val Ile Asn Asn Leu Gly Ile Glu His Ile Glu Tyr Arg Ser Glu Asn  
180 185 190

Ser Pro Asp Val Arg Pro Tyr Val Lys Gly Ile Arg Phe Glu Trp Val  
195 200 205

Arg Val Asp Leu Pro Glu Ile Tyr Lys Glu Val Arg Lys Leu Leu Arg  
210 215 220

Glu Met Leu Arg Asp Ala Leu Lys Pro Leu Ala Glu Thr Gly Leu Leu  
225 230 235 240

Glu Ser Ser Ser Pro Asp Ile Pro Lys Lys Glu Val Leu Arg Ala Gly  
245 250 255

Gln Ile Ile Asn Glu Glu Met Ala Lys Gly Asn His Asp Leu Arg Gly  
260 265 270

Leu Leu Leu Tyr His Ala Met Ala Leu Lys Leu His His Ala Ile Glu  
275 280 285

Leu Leu Glu Thr Gln Gly Leu Ser Ala Leu Arg Ala Tyr Ile Lys Lys  
290 295 300

Leu Tyr Glu Glu Ala Lys Ala Gly Ser Thr Lys Ala Ser Lys Glu Ile  
305 310 315 320

Phe Ser Asp Lys Arg Met Lys Lys Ala Ile Ser Leu Leu Val Gln Ala  
325 330 335

Lys Glu Ile Gly Leu Asp His Pro Lys Met Asp Lys Leu Lys Glu Ile  
340 345 350

Ile Arg Glu Gln Leu Gln Arg Lys Gln Asn Ser Lys Ile Ile Val Phe  
355 360 365

Thr Asn Tyr Arg Glu Thr Ala Lys Lys Ile Val Asn Glu Leu Val Lys  
370 375 380

Asp Gly Ile Lys Ala Lys Arg Phe Val Gly Gln Ala Ser Lys Glu Asn  
385 390 395 400

Asp Arg Gly Leu Ser Gln Arg Glu Gln Lys Leu Ile Leu Asp Glu Phe  
405 410 415

Ala Arg Gly Glu Phe Asn Val Leu Val Ala Thr Ser Val Gly Glu Glu  
420 425 430

Gly Leu Asp Val Pro Glu Val Asp Leu Val Val Phe Tyr Glu Pro Val  
435 440 445

Pro Ser Ala Ile Arg Ser Ile Gln Arg Arg Gly Arg Thr Gly Arg His  
450 455 460

Met Pro Gly Arg Val Ile Ile Leu Met Ala Lys Gly Thr Arg Asp Glu  
465 470 475 480

Ala Tyr Tyr Trp Ser Ser Arg Gln Lys Glu Lys Ile Met Gln Glu Thr  
485 490 495

Ile Ala Lys Val Ser Gln Ala Ile Lys Lys Gln Lys Gln Thr Ser Leu  
500 505 510

Val Asp Phe Val Arg Glu Lys Glu Ser Glu Lys Thr Ser Leu Asp Lys  
515 520 525

Trp Leu Lys Lys Glu Lys Glu Ala Thr Glu Lys Glu Glu Lys Lys  
530 535 540

Val Lys Ala Gln Glu Gly Val Lys Val Val Asp Ser Arg Glu Leu  
545 550 555 560

Arg Ser Glu Val Val Lys Arg Leu Lys Leu Leu Gly Val Lys Leu Glu  
565 570 575

Val Lys Thr Leu Asp Val Gly Asp Tyr Ile Ile Ser Glu Asp Val Ala  
580 585 590

Ile Glu Arg Lys Ser Ala Asn Asp Phe Ile Gln Ser Ile Ile Asp Gly  
595 600 605

Arg Leu Phe Asp Gln Val Lys Arg Leu Lys Glu Ala Tyr Ser Arg Pro  
610 615 620

Ile Met Ile Val Glu Gly Ser Leu Tyr Gly Ile Arg Asn Val His Pro  
625 630 635 640

Asn Ala Ile Arg Gly Ala Ile Ala Ala Val Thr Val Asp Phe Gly Val  
645 650 655

Pro Ile Ile Phe Ser Ser Thr Pro Glu Glu Thr Ala Gln Tyr Ile Phe  
660 665 670

Leu Ile Ala Lys Arg Glu Gln Glu Glu Arg Glu Lys Pro Val Arg Ile  
675 680 685

Arg Ser Glu Lys Lys Ala Leu Thr Leu Ala Glu Arg Gln Arg Leu Ile  
690 695 700

Val Glu Gly Leu Pro His Val Ser Ala Thr Leu Ala Arg Arg Leu Leu  
705 710 715 720

Lys His Phe Gly Ser Val Glu Arg Val Phe Thr Ala Ser Val Ala Glu  
725 730 735

Leu Met Lys Val Glu Gly Ile Gly Glu Lys Ile Ala Lys Glu Ile Arg  
740 745 750

Arg Val Ile Thr Ala Pro Tyr Ile Glu Asp Glu Glu  
755 760

<210> 78  
<211> 940  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Helicase 6

<400> 78  
Leu Lys Gly Leu Phe Arg Asp Val Ile Leu His Asn Pro His Leu Phe  
1 5 10 15  
Val Tyr Ser Tyr Ser Asp Lys Gly Ile Ile Pro Phe Lys His Gln Phe  
20 25 30  
Gln Thr Leu Tyr His Ala Met Leu Met Arg Pro Val Arg Leu Met Ile  
35 40 45  
Ala Asp Glu Ile Gly Leu Gly Lys Thr Ile Gln Ala Leu Leu Ile Ala  
50 55 60  
Lys Tyr Leu Asp Phe Arg Gly Glu Ile Glu Lys Ala Leu Ile Val Val  
65 70 75 80  
Pro Lys Val Leu Arg Glu Gln Trp Arg Glu Glu Val Lys Arg Ile Leu  
85 90 95  
Glu Glu Ala Pro Glu Val Ile Glu Asn Gly Ser Glu Ile Glu Trp Lys  
100 105 110  
Leu Lys Arg Pro Arg Lys Tyr Phe Ile Ile Ser Ile Asp Leu Ala Lys  
115 120 125  
Arg Tyr Thr Glu Glu Ile Leu Arg Gln Lys Trp Asp Leu Val Ile Val  
130 135 140  
Asp Glu Val His Asn Ala Thr Leu Gly Thr Gln Arg Tyr Glu Phe Leu  
145 150 155 160  
Lys Glu Leu Thr Lys Asn Lys Asp Leu Asn Val Ile Phe Leu Ser Ala  
165 170 175  
Thr Pro His Arg Gly Asn Asn Arg Asp Tyr Leu Ala Arg Leu Arg Leu  
180 185 190  
Leu Asp Pro Thr Ile Pro Glu Glu Ile Ser Pro Met His Glu Arg Lys  
195 200 205  
Ile Tyr Met Lys Ser Arg Gly Thr Leu Val Leu Arg Arg Thr Lys Lys  
210 215 220  
Val Val Asn Glu Leu Glu Gly Glu Val Phe Lys Lys Cys His Phe Gly  
225 230 235 240  
Ala Val Val Val Glu Val Ser Arg Glu Glu Arg Glu Phe Phe Glu Glu  
245 250 255  
Leu Asn Arg Ala Leu Phe Glu Leu Ile Lys Asp Gln Ala Asp Tyr Ser  
260 265 270  
Pro Leu Thr Leu Leu Ala Val Ile Ile Arg Lys Arg Ala Ser Ser Ser  
275 280 285  
Tyr Glu Ala Ala Leu Lys Thr Leu Thr Arg Ile Val Glu Ser Ala Tyr  
290 295 300  
Ile Ser Gly Gln Glu Arg Ala Arg Gly Val Glu Ser Tyr Ile Glu Lys

305 310 315 320  
Ile Phe Arg Met Gly Tyr Glu Glu Leu Glu Ile Glu Glu Phe Asn Glu  
325 330 335  
Ile Asp Asp Ala Ile His Lys Ile Ile Asp Glu Tyr Arg Gly Phe Leu  
340 345 350  
Thr Glu Glu Gln Leu Glu Arg Leu Arg Arg Val Leu Glu Leu Gly Lys  
355 360 365  
Lys Ile Gly Ser Lys Asp Ser Lys Leu Glu Val Ile Ser Asp Ile Val  
370 375 380  
Ala Tyr His Ile Arg Asn Gly Glu Lys Val Ile Ile Phe Thr Glu Phe  
385 390 395 400  
Arg Asp Thr Leu Glu Tyr Val Leu Glu Arg Leu Pro Asp Ile Leu Arg  
405 410 415  
Arg Lys His Gly Ile Val Leu Glu Lys Asp Asp Ile Ala Lys Leu His  
420 425 430  
Gly Gly Met Lys Ser Glu Glu Ile Glu Arg Glu Ile Asn Lys Phe His  
435 440 445  
Glu Arg Ala Asn Leu Leu Val Ser Thr Asp Val Ala Ser Glu Gly Leu  
450 455 460  
Asn Leu His Val Ala Ser Val Val Ile Asn Tyr Glu Ala Pro Trp Ser  
465 470 475 480  
Pro Ile Lys Leu Glu Gln Arg Val Gly Arg Ile Trp Arg Leu Asn Gln  
485 490 495  
Thr Arg Glu Thr Lys Ala Tyr Thr Ile Phe Leu Ala Thr Glu Thr Asp  
500 505 510  
Leu Asp Val Leu Asn Asn Leu Tyr Arg Lys Ile Met Asn Ile Lys Glu  
515 520 525  
Ala Val Gly Ser Gly Pro Ile Ile Gly Arg Pro Ile Phe Glu Gly Asp  
530 535 540  
Phe Glu Asn Leu Trp Asn Glu Gly Ala Glu Glu Glu Asn Arg Glu Val  
545 550 555 560  
Ser Glu Tyr Glu Leu Ile Leu Ala Ser Ile Lys Gly Glu Leu Lys Gly  
565 570 575  
Tyr Ala Gly Ala Leu Val Arg Thr Leu Arg Ile Leu Lys Gln Lys Val  
580 585 590  
Glu Gly Ala Val Pro Val Asn Pro Ala Gly Ser Ile Arg Arg Glu Leu  
595 600 605  
Glu Ile Ile Leu Glu Asp Thr Pro Asp Val Glu Val Leu Lys Lys Ile  
610 615 620  
Val Asn Arg Asn Val Pro Asn Pro Phe Arg Leu Val Arg Gly Leu Leu  
625 630 635 640

Arg Glu Ala Glu Gly Ile Glu Gly Ile Arg Val Leu Val Lys Gly Tyr  
645 650 655

Asp Gly Ser Met Asp Val Tyr Tyr Ala Ile Phe Tyr Asp Glu Asp Gly  
660 665 670

Arg Glu Ile Tyr Arg Tyr Pro Ile Leu Ala Glu Asn Gly Lys Tyr Leu  
675 680 685

Val Gly Phe Asn Leu Leu Lys Arg Ile Ser Glu Val Leu Ser Lys Glu  
690 695 700

Tyr Lys Val Val Arg Gly Ala Ser Glu Glu Val Asp Tyr Lys Val Lys  
705 710 715 720

Thr Leu Val Met Asp Asn Ile Tyr Asn Leu Ile Val Lys Lys Tyr Leu  
725 730 735

Glu Tyr Asp Ser Leu Asn Ile Lys Glu Gly Lys Ile Phe Lys Arg Leu  
740 745 750

Lys Val Glu Ile Lys Lys Ala Leu Glu Val Lys Gly Ile Ser Glu Glu  
755 760 765

Glu Phe Glu Val Ile Lys Arg Val Pro Pro Glu Ile Met Glu Val Leu  
770 775 780

Gly Leu Asp Ser Thr Lys Ile Glu Leu Pro Thr Asn Glu Tyr Leu Lys  
785 790 795 800

Ile Phe Glu Arg Asn Phe Val Pro Leu Asp Lys Ile Leu Glu Ser Glu  
805 810 815

Lys Lys Ala Met Glu Ile Val Met Glu Leu Glu Lys Ser Arg Gly Tyr  
820 825 830

Asn Val Glu Asp Val Ser Leu Arg Glu His Tyr Asp Ile Arg Ala Phe  
835 840 845

Thr Asp Gly Glu Glu Lys Tyr Ile Glu Val Lys Gly His Tyr Pro Met  
850 855 860

Leu Leu Leu Ala Glu Leu Thr Glu Lys Glu Phe Glu Phe Ala Gln Lys  
865 870 875 880

Asn Glu Asp Lys Tyr Trp Ile Tyr Ile Val Ser Asn Ile Ala Lys Asp  
885 890 895

Pro Val Ile Val Lys Ile Tyr Lys Pro Phe Ser Gln Asp Arg Arg Val  
900 905 910

Phe Val Val Lys Asn Gly Glu Asp Val Glu Val Asn Ile Asn Ile Glu  
915 920 925

Ile Lys Lys Lys Asp Arg His Leu Leu Lys Leu Ser  
930 935 940

<210> 79  
<211> 1278

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Helicase 7

<400> 79

Val Ile Thr Leu Glu Leu His Pro Ser Glu Ile Ala Arg Tyr Phe Glu  
1 5 10 15

Leu Glu Glu Cys Ser His Tyr Phe Ser Asn Leu Leu Leu Arg Lys Arg  
20 25 30

Gly Glu Leu Gln Glu Phe Glu Pro Ile Ile Arg Arg Lys Glu Ile Glu  
35 40 45

Thr Ile Glu Leu Ala Lys Trp Gly Asp Glu Phe Glu Leu Ser Leu Leu  
50 55 60

Gln Glu Phe Lys Lys Gly Glu Ala Leu Lys Lys Leu Gly Val Lys Glu  
65 70 75 80

Leu Pro Arg Phe Tyr Gly Phe Leu Thr Glu Asn Asp Thr Pro Val Arg  
85 90 95

Lys Phe Phe Glu Lys Tyr Phe Lys Asp Gly Ile Ile Val Glu Glu Asp  
100 105 110

Pro Asp Lys Leu Leu Glu Ile Ile Asn Ser Glu Lys Ser Ala Val Ile  
115 120 125

Tyr Gln Ala Pro Leu Lys Gly Arg Ile Gly Lys Phe Asp Val Ser Gly  
130 135 140

Arg Ala Asp Phe Ile Ile Lys Val Gly Lys Thr Leu Tyr Leu Leu Glu  
145 150 155 160

Ala Lys Phe Thr Lys Glu Glu Lys Phe Tyr His Arg Ile Gln Ala Ile  
165 170 175

Ile Tyr Ala His Leu Leu Ser Gln Met Ile Glu Gly Tyr Glu Ile Lys  
180 185 190

Leu Ala Val Val Thr Lys Glu Asn Phe Pro Ile Pro Ser Asn Phe Leu  
195 200 205

Arg Phe Pro Gly Asp Val Glu Glu Leu Lys Ile Thr Leu Glu Glu Lys  
210 215 220

Leu Gly Gly Ile Leu Arg Glu Gln Glu Leu Trp Ile Asp Ala Arg Cys  
225 230 235 240

Thr Thr Cys Pro Phe Glu Ala Leu Cys Leu Ser Lys Ala Leu Glu Glu  
245 250 255

Arg Ser Leu Gly Leu Leu Ser Leu Pro Pro Gly Ile Ile Arg Ile Leu  
260 265 270

Lys Glu Glu Gly Ile Lys Asp Leu Lys Asp Met Ala Lys Leu Phe Glu  
275 280 285

Phe Lys Glu Asn Ser Pro Thr Asn Phe Glu Glu Pro Ser Ile Lys Asp  
290 295 300

Pro Lys Lys Thr Gln Glu Ile Ala Lys Arg Thr Gly Ile Asn Leu Leu  
305 310 315 320

Lys Leu Ser Arg Ile Ala Gln Ala Ile Leu Lys Tyr Leu Asp Glu Gly  
325 330 335

Glu Thr Thr Pro Leu Phe Ile Pro Arg Thr Gly Tyr Asn Leu Pro Met  
340 345 350

Asp Glu Arg Val Gly Asp Val Glu Pro Ser Tyr Tyr Pro Pro Arg Ser  
355 360 365

Leu Val Lys Val Phe Phe Tyr Val Gln Thr Ser Pro Ile Thr Asp Thr  
370 375 380

Ile Ile Gly Ile Ser Ala Leu Val Lys Asn Arg Gln Asn Gly Glu Arg  
385 390 395 400

Ile Ile Val Lys Phe Val Asp Glu Pro Pro Ile Glu Val Ser Asp Ala  
405 410 415

Gln Glu Lys Glu Arg Met Leu Leu Ile Glu Phe Phe Arg Asp Val Ile  
420 425 430

Asp Ala Val Lys Ser Leu Ser Pro Thr Asp Lys Val Tyr Leu His Met  
435 440 445

Tyr Phe Tyr Asn Arg Lys Gln Arg Asp Asp Leu Met Asp Ala Val Lys  
450 455 460

Arg His Lys Glu Ile Arg Glu Asn Asn Ala Val Met Ala Leu Leu Ser  
465 470 475 480

Leu Arg Arg Ala Ile Asp Trp Glu Ser Phe Ser Ile Ile Lys Asp Glu  
485 490 495

Ile Ile Arg Arg His Ala Leu Pro Leu Ser Pro Gly Leu Gly Phe Val  
500 505 510

Thr Val Ala Thr Gln Phe Gly Tyr Arg Trp Arg Arg Asn Lys Thr Phe  
515 520 525

Ala Arg Met Leu Glu Val Val Ala Arg Arg Glu Asn Gly Lys Ile Asn  
530 535 540

Leu Lys Thr Leu Leu Asn Ile Ser Glu Thr Gly Ile Gly Pro Glu Tyr  
545 550 555 560

Tyr Pro Ile Ile Asp Arg Asp Asn Glu Gly Ile Pro Phe Thr Leu Phe  
565 570 575

Trp Ser Ala Leu Val Lys Leu Ala Thr Glu Glu Asp Asn Ser Arg Ile  
580 585 590

Lys Arg Asp Ile Arg Asp Ile Leu Ser Gln Met Val Glu Ala Leu Lys  
595 600 605

Thr Ile Glu Glu Arg Ile Pro Glu Gln Tyr Lys Asp Ala Phe Val Lys

610

615

620

Lys Glu Gly Ile Pro Lys Glu Asp Leu Glu Asn Phe Asp Ile Lys Lys  
625 630 635 640

Glu Glu Leu Ala Asp Ile Leu Leu Glu Tyr Leu Gln Leu Glu Phe Asp  
645 650 655

Ala Arg Phe Arg Glu Arg Ser Glu Tyr Tyr Arg Leu Pro Leu Ser Ile  
660 665 670

Arg Ala Tyr Ser Glu Glu Ser Ala Leu Ile Lys Ile Glu Asn Ile Glu  
675 680 685

Lys Lys Lys Asn Asp Cys Leu Leu Phe Gly Lys Ile Val Leu Ile Asp  
690 695 700

Glu Asn Gly Arg Ile Lys Glu Tyr Asn Pro Lys Glu Val Leu Ile Asp  
705 710 715 720

Ile Asp Glu Gly Ser Leu Val Val Val Thr Pro Lys Lys Phe Leu Asp  
725 730 735

Lys Leu Arg Arg Asp Pro Val Gln Arg Ile Ser Lys Ser Pro Leu Gly  
740 745 750

Ile Val Glu Ala Ile Asp His Glu Thr Gly Lys Val Val Ile Arg Leu  
755 760 765

Ile Arg Val Ser Pro Gly Arg Phe Thr Leu Lys His Ser Lys Phe Ser  
770 775 780

Cys Lys Asn Gly Leu Leu Thr Ile Thr Tyr Pro Glu Gly Glu Val Lys  
785 790 795 800

Val Thr Pro Gly Glu Ile Val Ile Val Asp Pro Ser Val Asp Asp Ile  
805 810 815

Gly Met Glu Arg Ala Tyr Asn Val Leu Ser Glu Ile Ser Gln Gly Glu  
820 825 830

Leu Lys His Glu Ile Tyr Gln Lys Val Lys Ala Ile Tyr Glu Gly Asn  
835 840 845

Thr Glu Ser Arg Tyr Glu Val Asn Ile Trp Lys Lys His Ile Glu  
850 855 860

Glu Phe Leu Ser Arg Val Lys Lys Ile Asn Glu Glu Gln Lys Lys Phe  
865 870 875 880

Ala Ile Asp Ile Asn Asn Phe Leu Val Thr Leu Gln Glu Pro Pro Gly  
885 890 895

Thr Gly Lys Thr Ser Gly Ala Ile Ala Pro Ala Ile Leu Ala Arg Ala  
900 905 910

Tyr Ser Met Val Lys Asp Lys Lys Asn Gly Leu Phe Val Val Thr Gly  
915 920 925

Val Ser His Arg Ala Val Asn Glu Ala Leu Ile Lys Thr Leu Lys Leu  
930 935 940

Lys Lys Glu Leu Glu Asn Thr Leu Lys Glu Leu Arg Lys Ile Asp Leu  
945 950 955 960

Ile Arg Ala Val Ser Gly Glu Glu Ala Ile Lys Ile Ile Lys Glu Glu  
965 970 975

Leu Glu Arg Glu Ile Lys Asp Asp Val Asp Arg Ile Arg Phe Thr Ala  
980 985 990

Gln Glu Ile Thr His Ser Ser Lys Gln Arg Ser Leu Asp Lys Tyr Phe  
995 1000 1005

Ala Asn Ser Gly Thr Val Arg Ile Val Phe Gly Thr Pro Gln Thr Leu  
1010 1015 1020

Asn Lys Leu Met Lys Asn Thr Lys Glu Val Glu Leu Val Val Ile Asp  
1025 1030 1035 1040

Glu Ala Ser Met Met Asp Leu Pro Met Phe Phe Leu Ser Thr Lys Val  
1045 1050 1055

Cys Lys Gly Gln Val Leu Leu Val Gly Asp His Arg Gln Met Glu Pro  
1060 1065 1070

Ile Gln Val His Glu Trp Gln Leu Glu Asp Arg Lys Thr Phe Glu Glu  
1075 1080 1085

His Tyr Pro Phe Leu Ser Ala Leu Asn Phe Ile Arg Phe Leu Arg Gly  
1090 1095 1100

Glu Leu Asp Glu Arg Glu Leu Lys Lys Phe Lys Arg Ile Leu Gly Arg  
1105 1110 1115 1120

Glu Pro Pro Glu Trp Lys Lys Asp Lys Asn Glu Val Leu Pro Leu Tyr  
1125 1130 1135

Arg Leu Val Arg Thr Tyr Arg Leu Pro Gln Glu Ile Ala Asp Leu Leu  
1140 1145 1150

Ser Asp Ala Ile Tyr Arg Ala Asp Gly Ile Lys Leu Ile Ser Glu Lys  
1155 1160 1165

Lys Lys Arg Arg Lys Ile Ile Ala Arg His Lys Asp Glu Phe Leu Ser  
1170 1175 1180

Ile Val Leu Asp Asp Arg Tyr Pro Phe Val Leu Ile Leu His Asp Glu  
1185 1190 1195 1200

Gly Asn Ser Thr Lys Ile Asn Glu Leu Glu Ala Lys Ile Val Glu Lys  
1205 1210 1215

Ile Ile Lys Arg Val Glu Asn Ile Asp Ile Gly Val Val Val Pro Tyr  
1220 1225 1230

Arg Ala Gln Lys Arg Leu Ile Ala Ser Leu Ile Asp Ser Ala Gln Val  
1235 1240 1245

Asp Thr Val Glu Arg Phe Gln Gly Gly Glu Lys Ser Leu Ile Val Ile  
1250 1255 1260

Ser Met Thr Ser Ser Asp Pro Arg Ile Pro Gly Lys Gly Phe  
1265 1270 1275

<210> 80  
<211> 655  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Helicase dna2

<400> 80  
Met Asn Ile Lys Ser Phe Ile Asn Arg Leu Lys Glu Leu Val Glu Ile  
1 5 10 15

Glu Arg Glu Ala Glu Ile Glu Ala Met Arg Leu Glu Met Lys Arg Leu  
20 25 30

Ser Gly Val Glu Arg Glu Arg Leu Gly Arg Ala Ile Leu Ser Leu Asn  
35 40 45

Gly Lys Ile Val Gly Glu Glu Leu Gly Tyr Phe Leu Val Lys Tyr Gly  
50 55 60

Arg Asn Lys Glu Ile Lys Thr Glu Ile Ser Val Gly Asp Leu Val Val  
65 70 75 80

Ile Ser Lys Arg Asp Pro Leu Lys Ser Asp Leu Leu Gly Thr Val Val  
85 90 95

Glu Lys Gly Lys Arg Phe Ile Val Val Ala Leu Glu Pro Val Pro Glu  
100 105 110

Trp Ala Leu Arg Asp Val Arg Ile Asp Leu Tyr Ala Asn Asp Ile Thr  
115 120 125

Phe Lys Arg Trp Ile Glu Asn Leu Asp Arg Val Arg Lys Ala Gly Lys  
130 135 140

Lys Ala Leu Glu Phe Tyr Leu Gly Leu Asp Glu Pro Ser Gln Gly Glu  
145 150 155 160

Glu Val Ser Phe Glu Pro Phe Asp Lys Ser Leu Asn Pro Ser Gln Arg  
165 170 175

Lys Ala Ile Ala Lys Ala Leu Gly Ser Glu Asp Phe Phe Leu Ile His  
180 185 190

Gly Pro Phe Gly Thr Gly Lys Thr Arg Thr Leu Val Glu Leu Ile Arg  
195 200 205

Gln Glu Val Lys Arg Gly Asn Lys Val Leu Ala Thr Ala Glu Ser Asn  
210 215 220

Val Ala Val Asp Asn Leu Val Glu Arg Leu Ala Lys Asp Gly Val Lys  
225 230 235 240

Ile Val Arg Val Gly His Pro Ser Arg Val Ser Arg His Leu His Glu  
245 250 255

Thr Thr Leu Ala Tyr Leu Ile Thr Gln His Glu Leu Tyr Gly Glu Leu  
260 265 270

Arg Glu Leu Arg Val Ile Gly Gln Ser Leu Ala Glu Lys Arg Asp Thr  
275 280 285

Tyr Thr Lys Pro Thr Pro Lys Phe Arg Arg Gly Leu Ser Asp Ala Glu  
290 295 300

Ile Ile Lys Leu Ala Glu Lys Gly Arg Gly Ala Arg Gly Leu Ser Ala  
305 310 315 320

Arg Leu Ile Lys Glu Met Ala Glu Trp Ile Lys Leu Asn Arg Gln Val  
325 330 335

Gln Lys Ala Phe Glu Asp Ala Arg Lys Leu Glu Glu Arg Ile Ala Arg  
340 345 350

Asp Ile Ile Arg Glu Ala Asp Val Val Leu Thr Thr Asn Ser Ser Ala  
355 360 365

Ala Leu Asp Val Val Asp Ala Thr Asp Tyr Asp Val Ala Ile Ile Asp  
370 375 380

Glu Ala Thr Gln Ala Thr Ile Pro Ser Ile Leu Ile Pro Leu Asn Lys  
385 390 395 400

Val Asp Arg Phe Ile Leu Ala Gly Asp His Lys Gln Leu Pro Pro Thr  
405 410 415

Ile Leu Ser Leu Glu Ala Gln Glu Leu Ser His Thr Leu Phe Glu Gly  
420 425 430

Leu Ile Glu Lys Tyr Pro Trp Lys Ser Glu Met Leu Thr Ile Gln Tyr  
435 440 445

Arg Met Asn Glu Arg Ile Met Glu Phe Pro Ser Arg Glu Phe Tyr Asp  
450 455 460

Gly Arg Ile Val Ala Asp Glu Ser Val Lys Asn Ile Thr Leu Ala Asp  
465 470 475 480

Leu Gly Ile Lys Val Asn Ala Ser Gly Ile Trp Arg Asp Ile Leu Asp  
485 490 495

Pro Asn Asn Val Leu Val Phe Ile Asp Thr Cys Met Leu Glu Asn Arg  
500 505 510

Phe Glu Arg Gln Arg Arg Gly Ser Glu Ser Arg Glu Asn Pro Leu Glu  
515 520 525

Ala Lys Ile Val Ser Lys Ile Val Glu Lys Leu Leu Glu Ser Gly Val  
530 535 540

Lys Ala Glu Met Met Gly Val Ile Thr Pro Tyr Asp Asp Gln Arg Asp  
545 550 555 560

Leu Ile Ser Leu Asn Val Pro Glu Glu Val Glu Val Lys Thr Val Asp  
565 570 575

Gly Tyr Gln Gly Arg Glu Lys Glu Val Ile Ile Leu Ser Phe Val Arg

580

585

590

Ser Asn Lys Ala Gly Glu Ile Gly Phe Leu Lys Asp Leu Arg Arg Leu  
595 600 605

Asn Val Ser Leu Thr Arg Ala Lys Arg Lys Leu Ile Met Ile Gly Asp  
610 615 620

Ser Ser Thr Leu Ser Ser His Glu Thr Tyr Arg Arg Leu Ile Glu His  
625 630 635 640

Val Arg Glu Lys Gly Leu Tyr Val Val Leu Thr Lys Asp Ser Ile  
645 650 655

<210> 81

<211> 2163

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant  
helicase 8

<400> 81

atgagggttg atgagctgag agttgatgag aggataaaaga gtactttgaa ggagagaggt 60  
atcgaatcct tttaccctcc ccaagccgag gccttaaaa gcccggatatt ggaaggtaag 120  
aatgcattaa ttcaattcc aacggccagc gggaaaaacac taattgctga gattgccccatg 180  
gttcatacgaa ttttgcacca gggagaaaag gctgtataca tagtcccgt gaaggccctg 240  
gctgaagaaa agtttcagga gttccaggat tgggagaaga ttgggttaag agtagcgatg 300  
gccactgggg attacgactc aaaggatgag tggttgggg aatacgcacat aatcattgcg 360  
acggctgaga agtttgattc ctttttaagg catggctcaa gttggattaa ggatgtgaag 420  
attttagttc ctgacgagat tcatttgatt gttcaagag acagaggagc tacgcttgc 480  
gttatcttag ctcatacgat cggaaaggcc caaataattt gactctctgc aacgatagga 540  
aatccagagg agcttgcgga gtggtaaat gcccgcataa tagtcagtga ctggaggccc 600  
gttaagcttta gaaggggagttttaacca ggccttgcata cctgggaaga tgaaagtata 660  
gacaggtttt cctcctggga agagtttagt tacgatgcac ttaggaagaa gaaaggagcg 720  
ctaattttttaa acatcgaa aaggaaggct gagagatgt ctggggagct ttctaaaaaa 780  
gttaagtctc tcctcacgaa acctgagatt agagttttaa atgaatttgc tgattccctc 840  
gaggaaaatcc cccacaaatgc aaagcttagt aaggccatata ggggtggagt tgcgttccac 900  
cacgctggtc ttggggagaga tgagagggtt ctcgtggagg agaactttttag aaagggtata 960  
ataaaggcccg tagttgccac cccaaacactt tcggcgggaa ttaacactcc agcgtttagg 1020  
gtgattataa gggatatttgc gaggactct gactttggaa tggagagaat tccgataatc 1080  
gaggttcacc aaatgcgttgc gagacttggaa aggccgaatg atgatgaggt tggggaggaa 1140  
ataatagttt ctacaagcga tgatccgaga gaggtatgc atcactacat atttggaaag 1200  
cctgaaaaac tggctccca gctctccaaac gagatatttgc tgagaagtca agttttggcc 1260  
ctaatacgca cctttggcttcaactgtg gaggagattt tgaagttcat ctcacacaca 1320  
ttctatgtttt atcaaaaggaa ggacacatac tcttttagagg agaagataag gaacataactc 1380  
tacttcctcc tagagaatgc gttcatagag atatccttag aggataaaat aaggccgtt 1440  
tccctggaa ttggactgc aaagctttaatcgtatccct atacggccaa gatgttcaag 1500  
gataaaatgg aggaagtgtt taaagatcca aatcctatacg aatatttca cttaaatctcc 1560  
ctaactccgg atataaaccctt cttcaactac tcaaagagag aatttggaaat gctcgaagag 1620  
gaataactacg aattcaagggaa tagtttatac tttgacgatc cttacatttc gggtaacgac 1680  
cccttacccatgg agaggaagttt cttcagatc ttcaaaaactgc cactatgtct tctggcatgg 1740  
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tataggatgttggagacggc tgagttgtg gtgtactctc taaaggaaat tgcaaaaagtt 1860  
cttggagctt atgagatcgat tggatattttt gaaacatttgc gggtagggat caagtatggg 1920  
attaggaggaa aattgattcc cttcaatgcac cttccgttgg ttggaaagaaag gagagctaga 1980  
gctcttaca atagcggatt tagaagtata gaggatataat ctcaagcggag gccagaagag 2040  
cttttggaaaatcgagggat aggggtcaag accgttggagg ctatcttcaa gtttcttgg 2100  
aagaatgtca aatattcggaa gaaacccatggaaaaaatgttactt tctcaatctc 2160

<210> 82  
<211> 720  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Recombinant  
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<400> 82  
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Lys Glu Arg Gly Ile Glu Ser Phe Tyr Pro Pro Gln Ala Glu Ala Leu  
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Lys Ser Gly Ile Leu Glu Gly Lys Asn Ala Leu Ile Ser Ile Pro Thr  
35 40 45  
  
Ala Ser Gly Lys Thr Leu Ile Ala Glu Ile Ala Met Val His Arg Ile  
50 55 60  
  
Leu Thr Gln Gly Gly Lys Ala Val Tyr Ile Val Pro Leu Lys Ala Leu  
65 70 75 80  
  
Ala Glu Glu Lys Phe Gln Glu Phe Gln Asp Trp Glu Lys Ile Gly Leu  
85 90 95  
  
Arg Val Ala Met Ala Thr Gly Asp Tyr Asp Ser Lys Asp Glu Trp Leu  
100 105 110  
  
Gly Lys Tyr Asp Ile Ile Ala Thr Ala Glu Lys Phe Asp Ser Leu  
115 120 125  
  
Leu Arg His Gly Ser Ser Trp Ile Lys Asp Val Lys Ile Leu Val Ala  
130 135 140  
  
Asp Glu Ile His Leu Ile Gly Ser Arg Asp Arg Gly Ala Thr Leu Glu  
145 150 155 160  
  
Val Ile Leu Ala His Met Leu Gly Lys Ala Gln Ile Ile Gly Leu Ser  
165 170 175  
  
Ala Thr Ile Gly Asn Pro Glu Glu Leu Ala Glu Trp Leu Asn Ala Glu  
180 185 190  
  
Leu Ile Val Ser Asp Trp Arg Pro Val Lys Leu Arg Arg Gly Val Phe  
195 200 205  
  
Tyr Gln Gly Phe Val Thr Trp Glu Asp Gly Ser Ile Asp Arg Phe Ser  
210 215 220  
  
Ser Trp Glu Glu Leu Val Tyr Asp Ala Ile Arg Lys Lys Lys Gly Ala  
225 230 235 240  
  
Leu Ile Phe Val Asn Met Arg Arg Lys Ala Glu Arg Val Ala Leu Glu  
245 250 255

Leu Ser Lys Lys Val Lys Ser Leu Leu Thr Lys Pro Glu Ile Arg Ala  
260 265 270

Leu Asn Glu Leu Ala Asp Ser Leu Glu Glu Asn Pro Thr Asn Glu Lys  
275 280 285

Leu Ala Lys Ala Ile Arg Gly Gly Val Ala Phe His His Ala Gly Leu  
290 295 300

Gly Arg Asp Glu Arg Val Leu Val Glu Glu Asn Phe Arg Lys Gly Ile  
305 310 315 320

Ile Lys Ala Val Val Ala Thr Pro Thr Leu Ser Ala Gly Ile Asn Thr  
325 330 335

Pro Ala Phe Arg Val Ile Ile Arg Asp Ile Trp Arg Tyr Ser Asp Phe  
340 345 350

Gly Met Glu Arg Ile Pro Ile Ile Glu Val His Gln Met Leu Gly Arg  
355 360 365

Ala Gly Arg Pro Lys Tyr Asp Glu Val Gly Glu Gly Ile Ile Val Ser  
370 375 380

Thr Ser Asp Asp Pro Arg Glu Val Met Asn His Tyr Ile Phe Gly Lys  
385 390 395 400

Pro Glu Lys Leu Phe Ser Gln Leu Ser Asn Glu Ser Asn Leu Arg Ser  
405 410 415

Gln Val Leu Ala Leu Ile Ala Thr Phe Gly Tyr Ser Thr Val Glu Glu  
420 425 430

Ile Leu Lys Phe Ile Ser Asn Thr Phe Tyr Ala Tyr Gln Arg Lys Asp  
435 440 445

Thr Tyr Ser Leu Glu Glu Lys Ile Arg Asn Ile Leu Tyr Phe Leu Leu  
450 455 460

Glu Asn Glu Phe Ile Glu Ile Ser Leu Glu Asp Lys Ile Arg Pro Leu  
465 470 475 480

Ser Leu Gly Ile Arg Thr Ala Lys Leu Tyr Ile Asp Pro Tyr Thr Ala  
485 490 495

Lys Met Phe Lys Asp Lys Met Glu Glu Val Val Lys Asp Pro Asn Pro  
500 505 510

Ile Gly Ile Phe His Leu Ile Ser Leu Thr Pro Asp Ile Thr Pro Phe  
515 520 525

Asn Tyr Ser Lys Arg Glu Phe Glu Arg Leu Glu Glu Glu Tyr Tyr Glu  
530 535 540

Phe Lys Asp Arg Leu Tyr Phe Asp Asp Pro Tyr Ile Ser Gly Tyr Asp  
545 550 555 560

Pro Tyr Leu Glu Arg Lys Phe Phe Arg Ala Phe Lys Thr Ala Leu Val  
565 570 575

Leu Leu Ala Trp Ile Asn Glu Val Pro Glu Gly Glu Ile Val Glu Lys

580

585

590

Tyr Ser Val Glu Pro Gly Asp Ile Tyr Arg Ile Val Glu Thr Ala Glu  
595 600 605

Trp Leu Val Tyr Ser Leu Lys Glu Ile Ala Lys Val Leu Gly Ala Tyr  
610 615 620

Glu Ile Val Asp Tyr Leu Glu Thr Leu Arg Val Arg Val Lys Tyr Gly  
625 630 635 640

Ile Arg Glu Glu Leu Ile Pro Leu Met Gln Leu Pro Leu Val Gly Arg  
645 650 655

Arg Arg Ala Arg Ala Leu Tyr Asn Ser Gly Phe Arg Ser Ile Glu Asp  
660 665 670

Ile Ser Gln Ala Arg Pro Glu Glu Leu Leu Lys Ile Glu Gly Ile Gly  
675 680 685

Val Lys Thr Val Glu Ala Ile Phe Lys Phe Leu Gly Lys Asn Val Lys  
690 695 700

Ile Ser Glu Lys Pro Arg Lys Ser Thr Leu Asp Tyr Phe Leu Lys Ser  
705 710 715 720

<210> 83

<211> 2163

<212> DNA

<213> Pyrococcus furiosus

<400> 83

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aatgcattaa ttcaattcc aacggccagc gaaaaaacac taattgctga gattgcattg 180  
gttcatagga ttttgcacca gggagggaaag gctgtataaca tagtcccgt gaaggccttg 240  
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acggctgaga agttgattt ccttttaagg catggctcaa gttggattaa ggatgtgaag 420  
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gttacccat ctcataatgct cggaaaggcc caaataattt gactctctgc aacgatagga 540  
aatccagagg agcttgcgga gtggtaaat gccgagctaa tagtcagtga ctggaggccc 600  
gttaagctt gaaggggagt ttttaccaa ggctttgtt cctgggaaga tggaaagtata 660  
gacagggtttt cctcctggga agagtttagt tacgatgcaa ttaggaagaa gaaaggagcg 720  
ctaattttt taaacatgag aaggaaggct gagagagtag ctttggagct ttctaaaaaa 780  
gttaagtc tccctcacgaa acctgagatt agagctttaa atgaatttgc tgattccctc 840  
gaggaaaaatc ccacaaatga aaagctagct aaggccattha ggggtggagt tgcgttccac 900  
cacgctggtc ttgggagaga tgagagggtt ctcgtggagg agaactttttag aaagggtata 960  
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gtgattataa gggatattt gggatattt gggatattt gactttggaa tggagagaat tccgataatc 1080  
gagggttacc aaatgcttgg gagagctgga aggccgaatg atgatgaggt tggggaggga 1140  
ataatagttt ctacaagcga tgatccgaga gaggtaatga atcactacat atttggaaag 1200  
cctgaaaaac tggctccca gctctccaaac gagagtaatt tgagaagtca agttttggcc 1260  
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gataaaatgg aggaagttgt taaagatcca aatcctataag gaatatttca cttaatctcc 1560  
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gaatactacg aattcaagga taggttatac tttgacgatc cttacatttc gggtaacgac 1680

ccctacctag agaggaagtt cttcagagct ttcaaaactg cactagtgct tctggcatgg 1740  
ataaaatgaag tcctcgaggg agaaatagtt gaaaagtact cggttggacc tggggacatc 1800  
tataggatag ttgagacggc tgagtggctg gtgtactctc taaaggaaat tgcaaaagtt 1860  
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gctcttaca atagcggatt tagaagtata gaggatata ctcaagcggag gccagaagag 2040  
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<210> 84  
<211> 720  
<212> PRT  
<213> Pyrococcus furiosus

<400> 84  
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Lys Glu Arg Gly Ile Glu Ser Phe Tyr Pro Pro Gln Ala Glu Ala Leu  
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Lys Ser Gly Ile Leu Glu Gly Lys Asn Ala Leu Ile Ser Ile Pro Thr  
35 40 45  
Ala Ser Gly Ile Leu Glu Ile Ala Glu Ile Ala Met Val His Arg Ile  
50 55 60  
Leu Thr Gln Gly Gly Lys Ala Val Tyr Ile Val Pro Leu Lys Ala Leu  
65 70 75 80  
Ala Glu Glu Lys Phe Gln Glu Phe Gln Asp Trp Glu Lys Ile Gly Leu  
85 90 95  
Arg Val Ala Met Ala Thr Gly Asp Tyr Asp Ser Lys Asp Glu Trp Leu  
100 105 110  
Gly Lys Tyr Asp Ile Ile Ala Thr Ala Glu Lys Phe Asp Ser Leu  
115 120 125  
Leu Arg His Gly Ser Ser Trp Ile Lys Asp Val Lys Ile Leu Val Ala  
130 135 140  
Asp Glu Ile His Leu Ile Gly Ser Arg Asp Arg Gly Ala Thr Leu Glu  
145 150 155 160  
Val Ile Leu Ala His Met Leu Gly Lys Ala Gln Ile Ile Gly Leu Ser  
165 170 175  
Ala Thr Ile Gly Asn Pro Glu Glu Leu Ala Glu Trp Leu Asn Ala Glu  
180 185 190  
Leu Ile Val Ser Asp Trp Arg Pro Val Lys Leu Arg Arg Gly Val Phe  
195 200 205  
Tyr Gln Gly Phe Val Thr Trp Glu Asp Gly Ser Ile Asp Arg Phe Ser  
210 215 220  
Ser Trp Glu Glu Leu Val Tyr Asp Ala Ile Arg Lys Lys Lys Gly Ala  
225 230 235 240

Leu Ile Phe Val Asn Met Arg Arg Lys Ala Glu Arg Val Ala Leu Glu  
245 250 255

Leu Ser Lys Lys Val Lys Ser Leu Leu Thr Lys Pro Glu Ile Arg Ala  
260 265 270

Leu Asn Glu Leu Ala Asp Ser Leu Glu Glu Asn Pro Thr Asn Glu Lys  
275 280 285

Leu Ala Lys Ala Ile Arg Gly Gly Val Ala Phe His His Ala Gly Leu  
290 295 300

Gly Arg Asp Glu Arg Val Leu Val Glu Glu Asn Phe Arg Lys Gly Ile  
305 310 315 320

Ile Lys Ala Val Val Ala Thr Pro Thr Leu Ser Ala Gly Ile Asn Thr  
325 330 335

Pro Ala Phe Arg Val Ile Ile Arg Asp Ile Trp Arg Tyr Ser Asp Phe  
340 345 350

Gly Met Glu Arg Ile Pro Ile Ile Glu Val His Gln Met Leu Gly Arg  
355 360 365

Ala Gly Arg Pro Lys Tyr Asp Glu Val Gly Glu Gly Ile Ile Val Ser  
370 375 380

Thr Ser Asp Asp Pro Arg Glu Val Met Asn His Tyr Ile Phe Gly Lys  
385 390 395 400

Pro Glu Lys Leu Phe Ser Gln Leu Ser Asn Glu Ser Asn Leu Arg Ser  
405 410 415

Gln Val Leu Ala Leu Ile Ala Thr Phe Gly Tyr Ser Thr Val Glu Glu  
420 425 430

Ile Leu Lys Phe Ile Ser Asn Thr Phe Tyr Ala Tyr Gln Arg Lys Asp  
435 440 445

Thr Tyr Ser Leu Glu Glu Lys Ile Arg Asn Ile Leu Tyr Phe Leu Leu  
450 455 460

Glu Asn Glu Phe Ile Glu Ile Ser Leu Glu Asp Lys Ile Arg Pro Leu  
465 470 475 480

Ser Leu Gly Ile Arg Thr Ala Lys Leu Tyr Ile Asp Pro Tyr Thr Ala  
485 490 495

Lys Met Phe Lys Asp Lys Met Glu Glu Val Val Lys Asp Pro Asn Pro  
500 505 510

Ile Gly Ile Phe His Leu Ile Ser Leu Thr Pro Asp Ile Thr Pro Phe  
515 520 525

Asn Tyr Ser Lys Arg Glu Phe Glu Arg Leu Glu Glu Glu Tyr Tyr Glu  
530 535 540

Phe Lys Asp Arg Leu Tyr Phe Asp Asp Pro Tyr Ile Ser Gly Tyr Asp  
545 550 555 560

Pro Tyr Leu Glu Arg Lys Phe Phe Arg Ala Phe Lys Thr Ala Leu Val  
565 570 575

Leu Leu Ala Trp Ile Asn Glu Val Pro Glu Gly Glu Ile Val Glu Lys  
580 585 590

Tyr Ser Val Glu Pro Gly Asp Ile Tyr Arg Ile Val Glu Thr Ala Glu  
595 600 605

Trp Leu Val Tyr Ser Leu Lys Glu Ile Ala Lys Val Leu Gly Ala Tyr  
610 615 620

Glu Ile Val Asp Tyr Leu Glu Thr Leu Arg Val Arg Val Lys Tyr Gly  
625 630 635 640

Ile Arg Glu Glu Leu Ile Pro Leu Met Gln Leu Pro Leu Val Gly Arg  
645 650 655

Arg Arg Ala Arg Ala Leu Tyr Asn Ser Gly Phe Arg Ser Ile Glu Asp  
660 665 670

Ile Ser Gln Ala Arg Pro Glu Glu Leu Leu Lys Ile Glu Gly Ile Gly  
675 680 685

Val Lys Thr Val Glu Ala Ile Phe Lys Phe Leu Gly Lys Asn Val Lys  
690 695 700

Ile Ser Glu Lys Pro Arg Lys Ser Thr Leu Asp Tyr Phe Leu Lys Ser  
705 710 715 720